

(19) World Intellectual Property Organization  
International Bureau(43) International Publication Date  
9 August 2001 (09.08.2001)

PCT

(10) International Publication Number  
WO 01/57276 A2(51) International Patent Classification<sup>7</sup>: C12Q 1/6894043 (US), RANK, David, R. [US/US]; 117 El Dorado  
Commons, Fremont, CA 94539 (US).

(21) International Application Number: PCT/US01/00668

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(22) International Filing Date: 30 January 2001 (30.01.2001)

(25) Filing Language: English

(26) Publication Language: English

## (30) Priority Data:

60/180,312	4 February 2000 (04.02.2000)	US
60/207,456	26 May 2000 (26.05.2000)	US
09/608,408	30 June 2000 (30.06.2000)	US
09/632,366	3 August 2000 (03.08.2000)	US
60/234,687	21 September 2000 (21.09.2000)	US
60/236,359	27 September 2000 (27.09.2000)	US
0024263.6	4 October 2000 (04.10.2000)	GB

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,  
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,  
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,  
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,  
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,  
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.(84) Designated States (*regional*): ARIPO patent (GH, GM,  
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian  
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European  
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,  
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,  
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## Published:

- without international search report and to be republished  
upon receipt of that report
- entirely in electronic form (except for this front page) and  
available upon request from the International Bureau

For two-letter codes and other abbreviations, refer to the "Guid-  
ance Notes on Codes and Abbreviations" appearing at the begin-  
ning of each regular issue of the PCT Gazette.(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE  
EXPRESSION IN HUMAN BONE MARROW(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene  
expression in a sample derived from human bone marrow is described. Also described are single exon nucleic acid probes expressed  
in the bone marrow and their use in methods for detecting gene expression.

WO 01/57276 A2

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW

CROSS REFERENCE TO RELATED APPLICATIONS

5 The present application is a continuation-in-part of U.S.  
patent application serial nos. 09/632,366, filed August 3,  
2000 and 09/608,408, filed June 30, 2000; claims the  
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent  
10 application serial nos. 60/236,359, filed September 27,  
2000, 60/234,687, filed September 21, 2000, 60/207,456,  
filed May 26, 2000, and 60/180,312, filed February 4, 2000;  
and further claims the benefit under 35 U.S.C. s 119(a) of  
UK patent application no. 0024263.6, filed October 4, 2000,  
15 the disclosures of which are incorporated herein by  
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY  
REFERENCE THEREOF

20 The present application includes a Sequence Listing in  
electronic format, filed pursuant to PCT Administrative  
Instructions 801 - 806 on a single CD-R disc, in  
triplicate, containing a file named pto\_BONE\_MARROW.txt,  
25 created 24 January 2001, having 26,421,347 bytes. The  
Sequence Listing contained in said file on said disc is  
incorporated herein by reference in its entirety.

Field of the Invention

30 The present invention relates to genome-derived  
single exon microarrays useful for verifying the expression  
of regions of genomic DNA predicted to encode protein. In  
particular, the present invention relates to unique genome-  
35 derived single exon nucleic acid probes expressed in human

bone marrow and single exon nucleic acid microarrays that include such probes.

### Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger *et al.*, *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert *et al.*, *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to  
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent  
15 biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via  
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick *et al.*, *Nature* 308(5955):153-8 (1984).

More recently, however, the development of high  
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein  
30 product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed  
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,  
Science 252:1651 (1991); Williamson, *Drug Discov. Today*  
4:115 (1999)). For nucleic acids sequenced by this  
approach, often the only biological information that is  
5 known *a priori* with any certainty is the likelihood of  
biologic expression itself. By virtue of the species and  
tissue from which the mRNA had originally been obtained,  
most such sequences are also annotated with the identity of  
the species and at least one tissue in which expression  
10 appears likely.

More recently, the pace of genomic sequencing has  
accelerated dramatically. When genomic DNA serves as the  
initial substrate for sequencing efforts, expression cannot  
be presumed; often the only *a priori* biological information  
15 about the sequence includes the species and chromosome (and  
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence  
accumulation by directed, EST, and genomic sequencing  
approaches – and in particular, with the accumulation of  
20 sequence information from multiple genera, from multiple  
species within genera, and from multiple individuals within  
a species – there is an increasing need for methods that  
rapidly and effectively permit the functions of nucleic  
sequences to be elucidated. And as such functional  
25 information accumulates, there is a further need for  
methods of storing such functional information in  
meaningful and useful relationship to the sequence itself;  
that is, there is an increasing need for means and  
apparatus for annotating raw sequence data with known or  
30 predicted functional information.

Although the increase in the pace of genomic  
sequencing is due in large part to technological changes in  
sequencing strategies and instrumentation, Service, *Science*  
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),  
35 there is an important functional motivation as well.



While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of  
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,  
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the  
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many  
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that  
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting  
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et  
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

*Ismb* 5:294-302 (1997); and GENESCAN, Burge *et al.*, *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset *et al.*, *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari *et al.*, *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon *et al.*, *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5           The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single  
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex  
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

          Because bone marrow is the tissue in which blood cells originate, diseases of the bone marrow are a significant cause of human morbidity and mortality.  
20 Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have in some cases been identified as causal - notably in the thalassemias and sickle cell anemia  
25 - disorders of the bone marrow are, for the most part, believed to have polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the bone marrow, particularly those diseases with polygenic etiology.

30

#### Summary of the Invention

          The present invention solves these and other problems in the art by providing methods and apparatus for  
35 predicting, confirming, and displaying functional

information derived from genomic sequence. The present invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

5           In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

10           The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

          Accordingly, in a first aspect of the invention,  
15 there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs:  
20 1 - 13,114 or a complementary sequence, or a portion of such a sequence.

          By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

25           In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

          In an alternative embodiment, each of said plurality of probes is separately and addressably  
30 isolatable from said plurality.

          In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

35           In yet another embodiment, said set of single

exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50; - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,012 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include

polymethylacrylic, polyethylene, polypropylene,  
polyacrylate, polymethylmethacrylate, polyvinylchloride,  
polytetrafluoroethylene, polystyrene, polycarbonate,  
polyacetal, polysulfone, celluloseacetate,  
5 cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

10 In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is  
15 packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression  
20 analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 13,115 - 26,012, wherein the fragment hybridizes at high stringency to an expressed human gene.  
25 In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,114.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from  
30 human bone marrow which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,114 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone  
35 marrow.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 13,115 - 26,012 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,013 - 38,628 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone marrow.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid

probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer; wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human bone marrow, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human bone marrow; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from



genomic sequence of said eukaryote; and then  
detecting specific hybridization of detectably  
labeled nucleic acids to a single exon probe,  
wherein said detectably labeled nucleic acids are  
5 derived from mRNA from the bone marrow of said eukaryote,  
said probe is a single exon probe having a fragment  
identical in sequence to, or complementary in sequence to,  
said predicted exon, said probe is included within a single  
exon microarray in accordance with the first aspect of the  
10 invention, and said fragment is selectively hybridizable at  
high stringency.

In a eighth aspect of the invention, there is  
provided a method of assigning exons to a single gene,  
comprising:

15 identifying a plurality of exons from genomic  
sequence in accordance with the seventh aspect of the  
invention; and then  
measuring the expression of each of said exons in  
a plurality of tissues and/or cell types using  
20 hybridization to single exon microarrays having a probe  
with said exon,  
wherein a common pattern of expression of said  
exons in said plurality of tissues and/or cell types  
indicates that the exons should be assigned to a single  
25 gene.

In an ninth aspect of the invention, there is  
provided a nucleic acid sequence as set out in any of SEQ  
ID NOS: 1 - 26,012 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is  
30 provided a peptide encoded by a sequence comprising a  
sequence as set out in any of SEQ ID NOS: 13,115 - 26,012,  
or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be  
encoded by a sequence comprising a sequence set out in any  
35 of SEQ ID NOS.: 1 - 13,114.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 26,013 - 38,628.

5           Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 26,013 - 38,628, or fragment thereof.

10           In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated  
15   sequence.

#### Detailed Description of the Invention

##### 20   Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately  
25   detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach  
30   (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the  
35   term "microarray" and phrase "nucleic acid microarray"

further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner  
5 *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid  
10 microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution  
15 phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the  
20 sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

25 As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop  
30 codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

35 As used herein the term "exon" refers to the

consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

5           As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons  
10 encoding the peptide are wholly contained within the exon.

          As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a  
15 nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

          As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present  
20 within a target mRNA.

          As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is  
25 meant that it is homologous to the given sequence.

          As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least  $10^7$ ,  
30 preferably at least  $10^8$ , more preferably at least  $10^9$  liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

          As used herein with respect to the visual display  
35 of annotated genomic sequence, the term "rectangle" means

any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

- 5           As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

10

#### Brief Description of the Drawings

- The present invention is further illustrated with reference to the following non-limiting figures and  
15 examples in which:

- FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in  
20 meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

- 25           FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

- FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length  
30 shown in black and PCR product length shown in dotted lines;

- FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color  
35 hybridization to a genome-derived single exon microarray.

The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

5           FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured  
10           tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

15           FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a  
20           BLAST Expect ("E") value of greater than  $1e-30$  ( $1 \times 10^{-30}$ ) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than  $1e-30$  ( $1 \times 10^{-30}$ ) ("known");

          FIG. 9 presents a Mondrian of BAC AC008172 (bases  
25           25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

          FIG. 10 is a Mondrian of BAC A049839.

30           Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

          FIG. 1 is a flow chart illustrating in broad  
35           outline a process for predicting functional regions from

genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original  
5 sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence  
10 data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will  
15 typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will  
20 minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically  
25 be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below.  
30 Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly  
35 include several divisions thereof, including the

- htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI).
- 5 Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.
- 10 Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to,
- 15 encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing
- 20 somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which

25 relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

- 30 Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic
- 35 assay. Where the subsequent experimental assay is



bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

5           The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

10           Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by  
15 incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for  
20 incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process  
25 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output  
30 from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational  
35 substrates for, and performance of subsequent assay, of

functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

5 Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to

10 process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be

15 identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction

20 analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of

25 sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend

30 upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the

35 sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were

static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query

20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS\_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or

codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified

within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after  
5 transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X  
10 chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment,  
15 for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described  
20 become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene  
25 prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and  
30 GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For  
35 the newly accessioned human genomic sequence input in

Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with  
5 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase  
10 reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

15 Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to  
20 process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report  
25 consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7%  
30 of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

35 Furthermore, consensus can be required among



different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process  
5 can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence,  
10 but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done  
15 in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process  
300 for identification of a subset thereof for functional  
20 assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental  
25 verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the  
30 species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

35 Where such subsequent gene expression assay uses

amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of

verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

5 Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is  
10 conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic)  
15 sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500  
20 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more  
25 effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400  
30 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs  
35 predicted from human genomic sequence according to the

methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at  
5 amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are  
10 thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no  
15 more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

20 Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit  
25 further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all  
30 amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not  
35 exceed about 25 nt in length. The "universal" priming

sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4<sup>th</sup> edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2<sup>nd</sup> edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

5           Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 10 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even 15 spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached 20 covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

25           Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources 30 (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays 35 typically also contain immobilized control nucleic acids.

For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or  
5 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural  
10 nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the  
15 immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates,  
20 the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed  
25 using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using  
30 nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid  
35 probe than can be achieved with spotting or lithography

techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such



microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the

desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include

artificial sequence similar to that found in EST  
microarrays. However, the genome-derived single exon  
microarray of the present invention can be made without  
such sequences, and if so constructed, presents an even  
5 smaller amount of nonspecific sequence that would  
contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned  
material as probes in EST microarrays is that such  
microarrays contain probes that result from cloning  
10 artifacts, such as chimeric molecules containing coding  
region of two separate genes. Derived from genomic  
material, typically not thereafter cloned, the probes of  
the genome-derived single exon microarrays of the present  
invention lack such cloning artifacts, and thus provide  
15 greater specificity of signal in gene expression  
measurements.

A further consequence of the cloned origin of  
probes on many EST microarrays is that the individual  
probes often have disparate sizes, which can cause the  
20 optimal hybridization stringency to vary among probes on a  
single microarray. In contrast, as discussed above, the  
probes arrayed on the genome-derived single exon  
microarrays of the present invention can readily be  
designed to have a narrow distribution in sizes, with the  
25 range of probe sizes no greater than about 10% of the  
average size, typically no greater than about 5% of the  
average probe size.

Because of their origin from fully- or partially-  
spliced message, probes disposed upon EST arrays will often  
30 include multiple exons. The percentage of such exon-  
spanning probes in an EST microarray can be calculated, on  
average, based upon the predicted number of exons/gene for  
the given species and the average length of the immobilized  
probes. For human genes, the near-complete sequence of  
35 human chromosome 22, Dunham et al., *Nature* 402(6761):489-95

(1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from  
5 algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-  
10 derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure  
15 tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in  
20 EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons  
25 for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic  
30 and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn  
35 from noncoding regions. As discussed above, the additional

presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

5           The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

10           Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization  
15 results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

          In contrast, the longer probe length of the  
20 genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or  
25 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

30           A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound  
35 noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence

drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-



transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is

disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation  
5 information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in  
10 international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should  
15 be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and  
20 characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic  
25 sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected  
30 of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,  
35 SAGE ("serial analysis of gene expression") databases, and

more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query -  
5 including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200,  
10 process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such  
15 annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or  
20 by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

25 The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the  
30 information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively  
35 described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the

sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from  
5 GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method  
10 and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to  
15 report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where  
20 display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by  
25 pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83  
30 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as  
35 many as can discriminably be displayed, depending upon the

number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions.

5 However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-  
10 selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted  
15 functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the  
20 results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function  
25 by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is  
30 protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe  
35 immobilized on the support surface of the microarray. As



noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

5           Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in  
10 process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically  
15 need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller  
20 rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880  
25 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

30           Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of  
35 rectangles 880 can be used to represent the degree of

sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as  
5 many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of  
10 expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which  
15 often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right  
20 borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical  
25 assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays,  
30 individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the  
35 spectra of the Cy3 and Cy5 dyes conventionally used for

respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,114 of these ORFs in bone marrow.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in bone marrow is currently available for use in measuring the level of its ORF's expression in bone marrow.

Because bone marrow is the tissue in which blood cells originate, diseases of the bone marrow are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations

in single genes have in some cases been identified as causal - notably in the thalassemias and sickle cell anemia - disorders of the bone marrow are, for the most part, believed to have polygenic etiologies.

5           For example, cancers that originate in the bone marrow and lymphatic tissues such as the lymphomas, leukemias, and myeloma have been recognized as a major health concern. An estimated 632,000 Americans are presently living with lymphoma, leukemia or myeloma, and  
10 over 110,000 new cases are anticipated each year. The new cases alone account for 11% of all cancer cases reported in the United States.

          Lymphoma is a general term for a group of cancers of lymphocytes that manifest in the tissues of the  
15 lymphatic system. Eventually, monoclonal proliferation crowds out healthy cells and creates tumors which enlarge lymph nodes. Approximately 450,000 members of the U.S. population are living with lymphoma: 160,000 with Hodgkin disease (HD) and 290,000 with non-Hodgkin lymphoma.

20           Hodgkin disease (HD) is a specialized form of lymphoma, and represent about 8% of all lymphomas. HD can be distinguish in tissues by the presence of an abnormal cell called the Reed-Sternberg cell. Incidence rates of HD are higher in adolescents and young adults, but HD is  
25 considered to be one of the most curable forms of cancer. Symptoms of HD include painless swelling of lymph glands, fatigue, recurrent high fever, sweating at night, skin irritations and loss of weight.

          Although an infectious etiology has been proposed  
30 to account for the disproportionate incidence of HD among siblings reared together - particularly an association with Epstein Barr Virus (EBV) - multiple genetic contributions have also been suggested.

          As early as 1986, linkage to HLA was suggested,  
35 with Klitz et al., Am. J. Hum. Genet. 54: 497-505 (1994)

reporting an overall association of the nodular sclerosing (NSHD) group with the HLA class II region. Results of the study suggested that susceptibility to NSHD is influenced by more than 1 locus within the class II region. Through a literature search, Shugart and Collins (2000), *Europ. J. Hum. Genet.* 8: 460-463 (2000), performed a combined segregation and linkage analysis on 59 nuclear families with HD and concluded that HD is most likely determined by both an HLA-associated major gene and other non-HLA genetic factors, in conjunction with environmental effects.

Non-Hodgkin lymphoma (NHL) is a malignant monoclonal proliferation of the lymphoid cells in the immune system, including bone marrow, spleen, liver and GI tract. The pathologic classification of NHL continues to evolve, reflecting new insights into the cells of origin and the biologic bases of these heterogeneous diseases. The course of NHL varies from indolent and initially well tolerated to rapidly fatal. Furthermore, common clinical symptoms of NHL, but rare in HD, are congestion and edema of the face and neck and ureteral compression.

Non-Hodgkin lymphoma (NHL) has been linked to a variety of specific genetic defects, including 26 mutated genes and at least 9 identified chromosomal translocations. Among the mutated genes are: ALK (2p23); API2 (MIHC, cIAP2) (11q22-q23); API4 (survivin, SVV) (17q25(?)); ATM (ATA, ATC) (11q22.3); BCL1 (11q13.3); BCL10 (CLAP, CIPER) (1p22); BCL2 (18q21.3); BCL6 (LAZ3, ZNF51) (3q27); BLYM (1p32); BMI1 (10p13); CCND1 (D11S287E, Cyclin D, PRAD1) (11q13); CD44 (MDU3, HA, MDU2) (11pter-p13); FRAT1 (10q23-q24(?)); FRAT2 (GBP) (10(?)); IL6 (IFNB2) (7p21); IRF4 (MUM1, LSIRF) (6p25-p23); LCP1 (PLS2) (13q14.1-q14.3); MALT1 (MLT) (18q21); MUC1 (PUM, PEM) (1q21); MYBL1 (AMYB, A-MYB) (8q22); MYC (CMYC, C-MYC) (8q24.12-q24.13); NBS1 (8q21); NPM1 (B23) (5q35); PCNA (20p12); TIAM1 (21q22.1); and TP53 (p53, P53) (17q13.1).

Among the chromosomal abnormalities are: t(1;14)

(p22;q32); t(14;18)(q32;q21); t(3;14)(q27;q32);  
t(6;14)(p25;q32); t(11;18)(q21;q21); t(1;14)(q21;q32);  
t(2;5)(p23;q35); add(14q32) / dup(14p32); and  
t(11;14)(q13;q32).

5 Additional genetic loci, as yet undiscovered, are  
believed to account for other occurrences of NHL.

As another example, acute leukemia is a malignant  
disease of blood-forming tissues such as the bone marrow.  
It is characterized by the uncontrolled growth of white  
10 blood cells. As a result, immature myeloid cells (in acute  
myelogenous leukemia (AML)) or lymphoid cells (in acute  
lymphocytic leukemia (ALL)) rapidly accumulate and  
progressively replace the bone marrow; diminished  
production of normal red cells, white cells, and platelets  
15 ensues. This loss of normal marrow function in turn gives  
rise to the typical clinical complications of leukemia:  
anemia, infection, and bleeding.

If untreated, ALL is rapidly fatal; most patients  
die within several months of diagnosis. With appropriate  
20 therapy, many patients can be cured. The survival rate for  
patients diagnosed with AML or ALL is 14% and 58%  
respectively. However, the incidences of AML is expected  
to be greater than ALL: an estimated 10,000 new cases of  
AML, predominantly in older adults, is anticipated in the  
25 U.S. alone, whereas 3,100 new cases of ALL are expected,  
with 1,500 of these new cases occurring among children.

The etiology of acute leukemia is not known.  
Although human T-cell lymphotropic virus type I (HTLV-I), a  
causative agent of adult T-cell leukemia, and HTLV-II,  
30 obtained from several patients with a syndrome resembling  
hairy cell leukemia, have been isolated, the etiologic link  
between HTLV and malignancy is uncertain. There is,  
however, evidence which suggests a genetic predisposition  
to incidences of acute leukemia.

35 For example, genetic disorders such as Fanconi

anemia and Down syndrome appear to increase risk of acute leukemia, specifically, AML. Evidence supporting a chromosome 21 locus for acute myelogenous leukemia (AML) includes the finding of linkage to 21q22.1-q22.2 in a  
5 family with a platelet disorder and propensity to develop AML (Ho et al., Blood 87: 5218-5224 (1996), an increased incidence of leukemia in Down syndrome, and frequent somatic translocation in leukemia involving the CBFA gene on 21q22.3. In addition, Horwitz et al., Am. J. Hum.  
10 Genet. 61:873-881 (1997), suggest that a gene on 16q22 may be a second cause of acute myelogenous leukemia. Nonparametric linkage analysis gave a P-value of 0.00098 for the conditional probability of linkage. Mutational analysis excluded expansion of the AT-rich minisatellite  
15 repeat FRA16B fragile site and the CAG trinucleotide repeat in the E2F-4 transcription factor. Large CAG repeat expansion was excluded as a cause of leukemia in this family.

Similarly, acute lymphoblastic leukemia (ALL) has  
20 been suggested to have a genetic predisposition. In particular, linkage to chromosome 9p has been reported by a number of groups. Chilcote et al., New Eng. J. Med. 313: 286-291 (1985), found that 6 of 8 patients with clinical features of lymphomatous ALL (LALL), a distinct category of  
25 ALL of T-cell lineage, had karyotypic abnormalities leading to loss of bands 9p22-p21. The mechanisms varied and included deletions, unbalanced translocations, and loss of the entire chromosome; only 1 of 57 patients without LALL had an abnormality of chromosome 9 at diagnosis. Kowalczyk  
30 et al., Cancer Genet. Cytogenet. 9:383-385 (1981), had earlier found changes in 9p in a subgroup of ALL cases. Chilcote et al. (1985) pointed out that there is a fragile site at 9p21 and raised the question of familial predisposition on this basis. This fragile site is the  
35 breakpoint in the translocation t(9;11)(p21-22;q23), which



is associated with acute nonlymphocytic leukemia with monocytic features, ANLL-AMoL-M5a. In a large series, Murphy et al., New Eng. J. Med. 313:1611 (1985), confirmed an abnormality of 9p in 10 to 11% of cases (33 out of more than 300) of acute lymphoblastic leukemia. The breakpoints in 9p clustered in the p22-p21 region. They could not, however, corroborate the specific association with T-cell origin or so-called lymphomatous clinical features. In addition, Taki et al., Proc. Natl. Acad. Sci. USA 96:14535 (1999), recently identified AF5q31, a new AF4-related gene, fused to MLL in infant ALL with ins(5;11)(q31;q13q23), and suspects that AF5q31 and AF4 might define a new family particularly involved in the pathogenesis of 11q23-associated-ALL.

As yet a further example of a disease affecting bone marrow with likely polygenic etiology is multiple myeloma (MM).

MM is a cancer of plasma cells, the final differentiated stage of B lymphocyte maturation. The malignant clone proliferates in the bone marrow and frequently invades the adjacent bone, producing extensive skeletal destruction that results in bone pain and fractures. Anemia, hypercalcemia, and renal failure are some clinical manifestations associated with MM.

MM causes 1% of all cancer deaths in Western countries. A genetic component to its etiology is suggested by disparate incidence among various groups in the country. Its incidence is higher in men than in women, in people of African descent relative to the U.S. population at large, and in older adults as compared to the young. It has been estimated that 14,000 new cases of myeloma will be diagnosed in the U.S., and over 11,000 persons will die from MM within the year.

Although, Kaposi's sarcoma-associated herpes virus has been associated with MM (Retig et al., Science

276:1851 (1997)), there is evidence that chromosomal abnormalities, such as the deletion of 13q14 and rearrangements of 14q increase the proliferation of myeloma cells.

5 Up to 30% of patients who suffer with MM have a balanced translocation, t(4;14)(p16.3;q32), that places the fibroblast growth factor receptor 3 (FGFR3) gene under the control of IgH promoter elements (Chesi et al., Nat. Genet. 16:260 (1997)). This results in increased expression of  
10 FGFR3, a member of a family of tyrosine kinase receptors implicated in control of cellular proliferation.

According to Zoger et al., Blood 95:1925 (2000), monoallelic deletions of the retinoblastoma-1 (rb-1) gene and the D13S319 locus were observed in 48 of 104 patients  
15 (46.2%) and in 28 of 72 (38.9%) patients, respectively, with newly diagnosed MM. Fluorescence in situ hybridization (FISH) studies found that 13q14 was deleted in all 17 patients with karyotypic evidence of monosomy 13 or deletion of 13q but also in 9 of 19 patients with  
20 apparently normal karyotypes. Patients with a 13q14 deletion were more likely to have higher serum levels of beta(2)-microglobulin (P=0.059) and a higher percentage of bone marrow plasma cells (P=0.085) than patients with a normal 13q14 status on FISH analysis. In patients with a  
25 deletion of 13q14, myeloma cell proliferation was markedly increased. The presence of a 13q14 deletion on FISH analysis was associated with a significantly lower rate of response to conventional-dose chemotherapy (40.8% compared with 78.6%; P =.009) and a shorter overall  
30 survival (24.2 months compared with > 60 months; P <.005) than in patients without the deletion.

There are numerous other mutated genes and chromosomal abnormalities that may predispose to MM. Examples of such genes are: B2M (15q21-q22); CCND1  
35 (D11S287E, Cyclin D, PRAD1)(11q13); CD19 (16p11.2 ); HGF

(HPTA) (7q21.1); IL6 (IFNB2) (7p21); IRF4 (MUM1, LSIRF) (6p25-p23); LTA (TNFB, LT) (6p21.3); SDC1 (2p24.1); and TNF (TNFA, TNFSF2, DIF) (6p21.3). Examples of chromosomal abnormalities include: t(6;14) (p25;q32) and  
5 t(11;14) (q13;q32).

Other significant diseases or disorders of the bone marrow are also believed, or likely to have, a genetic, typically polygenic, etiologic component. These diseases include, for example, chronic myeloid leukemia,  
10 chronic lymphoid leukemia, polycythemia vera, myelofibrosis, primary thrombocythemia, myelodysplastic syndromes, Wiskott-Aldrich, lymphoproliferative syndrome, aplastic anemia, Fanconi anemia, Down syndrome, sickle cell disease, thalassemia, granulocyte disorders, Kostmann  
15 syndrome, chronic granulomatous disease, Chediak-Higashi syndrome, platelet disorders, Glanzmann thrombasthenia, Bernard-Soulier syndrome, metabolic storage diseases, osteoporosis, congenital hemophagocytic syndrome.

The human genome-derived single exon nucleic acid  
20 probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human bone marrow, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be expressed  
25 at detectable levels in human bone marrow, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, diagnosis, grading, and/or staging  
30 of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of a given bone marrow disease, or to specific grades or stages thereof.

35 In one embodiment, the patient gene expression

profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the patient's bone marrow (or cells cultured therefrom) to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the bone marrow of individuals with known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of diseases of bone marrow to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human bone marrow. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the bone marrow has been demonstrated are useful for both measurement in the bone marrow and for survey of expression in other tissues.

Significant among such advantages is the presence

of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc.*

- Natl. Acad. Sci. USA 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).
- Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer

Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold *et al.*, *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena *et al.*

The invention particularly provides genome-derived single-exon probes known to be expressed in bone marrow. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity

sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA  
5 complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as  
10 complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

15 Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity  
20 suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and  
25 WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

30 Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or  
35 100 pg or more.



Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however — that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) — length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable

of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are  
5 required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,115 - 26,012, respectively, for probe SEQ ID  
10 NOS. 1 - 13,114. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,115 - 26,012 individually  
15 by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency  
20 conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c<sub>ot</sub>1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20  
25 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as  
30 the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes  
35 of the present invention is dictated by the proximity of

other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one  
5 expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more  
10 usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand  
15 of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art  
20 to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to  
25 provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic  
30 and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

35 And when intended for use in solution

hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as  $^3\text{H}$ ,  $^{32}\text{P}$ ,  $^{33}\text{P}$ ,  $^{35}\text{S}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ; fluorescent  
5 labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR®

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates  
10 thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

15 The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived  
20 single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96  
25 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3'  
30 primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon  
35 probes can usefully include a plurality of probes chosen

for the common attribute of expression in the human bone marrow.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be  
5 chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be  
10 used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

15 It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

20 The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human bone marrow. In preferred embodiments, the present invention provides human genome-derived single exon microarrays  
25 comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 13,114.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived  
30 single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression  
35 measurements. Alternatively, at a given probe density, the

same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,114 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,115 - 26,012, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,114 can be used, or that portion thereof in SEQ ID NOS. 13,115 - 26,012 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT<sup>™</sup> Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X<sup>™</sup> Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL<sup>™</sup>) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis

(Oxford Chemistry Primers, No 7) , Oxford Univ. Press  
(August 1992) (ISBN: 0198556683); and Bodanszky, Principles  
of Peptide Synthesis (Springer Laboratory), Springer Verlag  
(December 1993) (ISBN: 0387564314).

5           It is, therefore, another aspect of the invention  
to provide peptides comprising an amino acid sequence  
translated from SEQ ID NOS.: 13,115 - 26,012. Such amino  
acid sequences are set out in SEQ ID NOS: 26,013 - 38,628.  
Any such recombinantly-expressed or synthesized peptide of  
10 at least 8, and preferably at least about 15, amino acids,  
can be conjugated to a carrier protein and used to generate  
antibody that recognizes the peptide. Thus, it is a  
further aspect of the invention to provide peptides that  
have at least 8, preferably at least 15, consecutive amino  
15 acids.

The following examples are offered by way of  
illustration and not by way of limitation.

#### 20 EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted  
in Human Genomic Sequence

#### Bioinformatics Results

25           All human BAC sequences in fewer than 10 pieces  
that had been accessioned in a five month period  
immediately preceding this study were downloaded from  
GenBank. This corresponds to ~2200 clones, totaling ~350  
MB of sequence, or approximately 10% of the human genome.

30           After masking repetitive elements using the  
program CROSS\_MATCH, the sequence was analyzed for open  
reading frames using three separate gene finding programs.  
The three programs predict genes using independent  
algorithmic methods developed on independent training sets:  
35 GRAIL uses a neural network, GENEFINDER uses a hidden

Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic  
5 DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION  
10 yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three  
15 programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs  
20 ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single  
25 gene if fewer than 7 exons were found within the 25 kb window.

#### PCR

The largest ORF from each gene bin that did not  
30 span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments  
35 fewer than 250 bp in length do not bind well to the amino-



modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

- 5                   Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ). A first  
10 additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing  
15 the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

- The ORFs were then PCR amplified from genomic  
20 DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

- Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard  
25 techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR<sup>®</sup> green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR  
30 amplification was classified as successful if a single band appeared.

- The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon)  
35 length and distribution of amplified PCR products, with ORF

length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median  
5 size of 150 bp (n=9498). With an average amplicon size of  $475 \pm 25$  bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

10           Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of  
15 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

          Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were  
20 sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

          Some genomic clones (BACs) yielded very poor PCR  
25 and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

          Although the intronic and intergenic material  
30 flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was  
35 similarly found not to affect differential expression

ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-  
5 described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally  
10 included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt  
15 GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than  $1 \text{ e}^{-100}$ ) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe  
20 sequences showed some homology to a known EST or mRNA (BLAST E values from  $1 \text{ e}^{-5}$  to  $1 \text{ e}^{-99}$ ). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

25 All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are  
30 presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis
--

Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

## EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

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The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message

pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

- 5 Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA<sup>+</sup> mRNA performed using 1 µg oligo(dT)12-18 primer  
10 and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM  
15 Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup  
20 column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

- Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a  
25 Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c<sub>ot</sub>1 DNA, and 0.5 % SDS.

- Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C  
30 overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

- 35 Slides were scanned using a Molecular Dynamics

Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

5           Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of  
10 at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

15           Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

          The relative expression signal for these probes  
20 was then plotted as function of tissue or cell type, and is presented in FIG. 6.

          FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not  
25 expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

          Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed"  
30 products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were  
35 expressed in all 10 tissues. The next most common class

(15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are  
5 compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is  
10 represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than  
15 "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is  
20 novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that  
25 were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100;  
30 HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose  
35 expression was measurable in only a single of the tested

tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

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#### Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e-30$  (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than  $1e-30$  ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes



will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for  
5 incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

#### Verification of Gene Expression

10 To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

15 Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR  
20 against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300\_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence  
25 AL031734\_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue  
30 type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However,  
35 in addition to the two RT-PCR results presented above, the

observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

20

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normalized Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca <sup>2+</sup> binding protein expressed in central nervous

				system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to

				the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be  
5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B  $\text{Ca}^{2+}$  binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097  
10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3  
15 were both found to be phosphatases present in neurons (Millward *et al.*, *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed

down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 $\alpha$  (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in

choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	$-1.81 \pm 0.11$	$-1.85 \pm 0.08$
Brain	$-1.41 \pm 0.11$	$-1.17 \pm 0.05$
BT474	$1.85 \pm 0.09$	$1.66 \pm 0.12$
Fetal Liver	$-1.62 \pm 0.07$	$-1.41 \pm 0.05$
HBL100	$1.32 \pm 0.05$	$2.64 \pm 0.12$
Heart	$1.16 \pm 0.09$	$1.56 \pm 0.10$
HeLa	$1.11 \pm 0.06$	$1.30 \pm 0.15$
Liver	$-1.62 \pm 0.22$	$-2.07 \pm$
Lung	$-4.95 \pm 0.93$	$-3.75 \pm 0.21$
Placenta	$-3.56 \pm 0.25$	$-3.52 \pm 0.43$

10

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

20 EXAMPLE 3

Representation of Sequence and Expression Data as a  
"Mondrian"

For each genomic clone processed for microarray  
5 as above-described, a plethora of information was  
accumulated, including full clone sequence, probe sequence  
within the clone, results of each of the three gene finding  
programs, EST information associated with the probe  
sequences, and microarray signal and expression for  
10 multiple tissues, challenging our ability to display the  
information.

Accordingly, we devised a new tool for visual  
display of the sequence with its attendant annotation  
which, in deference to its visual similarity to the  
15 paintings of Piet Mondrian, is hereinafter termed a  
"Mondrian". FIGS. 3 and 4 present the key to the  
information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases  
25,000 to 130,000 shown), containing the carbamyl phosphate  
20 synthetase gene (AF154830.1). Purple background within the  
region shown as field 81 in FIG. 3 indicates all 37 known  
exons for this gene.

As can be seen, GRAIL II successfully identified  
27 of the known exons (73%), GENEFINDER successfully  
25 identified 37 of the known exons (100%), while DICTION  
identified 7 of the known exons (19%).

Seven of the predicted exons were selected for  
physical assay, of which 5 successfully amplified by PCR  
and were sequenced. These five exons were all found to be  
30 from the same gene, the carbamyl phosphate synthetase gene  
(AF154830.1).

The five exons were arrayed, and gene expression  
measured across 10 tissues. As is readily seen in the  
Mondrian, the five chip sequences on the array show  
35 identical expression patterns, elegantly demonstrating the

reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom): red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); turquoise =  $\alpha$ 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

#### EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in bone marrow tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical



structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the  
5 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,114 single exon probes, each fragment corresponding to an extension product from one of  
10 the two amplification primers.)

The structures of the 13,114 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,114 . The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not  
15 included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,115 - 26,012, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than  
20 one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant  
25 expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give  
30 a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the  
35 population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining  
5 control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations)  
10 are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean +  
15 (3\*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any  
20 signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human bone marrow and thus  
25 presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human bone marrow tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,115 - 26,012 was individually  
30 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were  
35 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe: "EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs

in an exhaustive process based on the following criteria:

1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all  
5 of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion  
10 of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about  $1e-05$  and  $1e-100$ ), the descriptor reveals the likely function of the  
15 protein encoded by the probe's ORF.

Using BLAST E value cutoffs of  $1e-05$  (i.e.,  $1 \times 10^{-5}$ ) and  $1e-100$  (i.e.,  $1 \times 10^{-100}$ ) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of  $1e-30$  was used as  
20 the boundary when only two classes were to be defined for analysis (unknown,  $>1e-30$ ; known  $<1e-30$ ) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about  $1e-100$  - which is probative evidence that the query sequence has previously  
25 been shown to be expressed - the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even  
30 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent  
35 a proper subset of the data present within the attached

sequence listing. For each amplicon probe (SEQ ID NOS.: 1 - 13,114) and probe exon (SEQ ID NOS.: 13,115 - 26,012, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

- 5           (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;
- (b) the most similar sequence provided by BLAST
- 10       query of the EST database, with accession number and BLAST E value for the "hit";
- (c) the most similar sequence provided by BLAST
- query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and
- 15       (d) the most similar sequence provided by BLASTX
- query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

#### 20   EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring  
Expression of Genes in Human Bone marrow

- Table 4 (546 pages) presents expression, homology, and
- 25   functional information for the genome-derived single exon probes that are expressed significantly in human bone marrow.

30

## CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived  
5 from human bone marrow comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 13,114 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid  
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid  
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 13,115 - 26,012.
5. A spatially-addressable set of single exon nucleic acid  
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid  
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid  
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,114 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human bone marrow.

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14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 13,115 - 26,012 or a complementary sequence or a fragment thereof.
- 5
15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any  
10 of SEQ ID NOs.: 26,013 - 38,628, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone marrow.
- 15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
- 20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.
18. A single exon nucleic acid probe as claimed in any one  
25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.
19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.
- 30
20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
- 35 21. A single exon nucleic acid probe as claimed in any one



of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample  
5 derived from human bone marrow, comprising:  
    contacting the microarray of claim 12, with a first  
        collection of detectably labeled nucleic acids,  
        said first collection of nucleic acids derived  
        from mRNA of human bone marrow; and then  
10 measuring the label detectably bound to each probe of  
    said microarray.

23. A method of identifying exons in a eukaryotic genome,  
comprising:  
15 algorithmically predicting at least one exon from  
    genomic sequence of said eukaryote; and then  
    detecting specific hybridization of detectably labeled  
    nucleic acids to a single exon probe,  
wherein said detectably labeled nucleic acids are derived  
20 from mRNA from the bone marrow of said eukaryote, said  
probe is a single exon probe having a fragment identical in  
sequence to, or complementary in sequence to, said  
predicted exon, said probe is included within a microarray  
according to claim 12, and said fragment is selectively  
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,  
comprising:  
    identifying a plurality of exons from genomic  
30 sequence according to the method of claim 23; and  
    then  
    measuring the expression of each of said exons in a  
    plurality of tissues and/or cell types using  
    hybridization to single exon microarrays having a  
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 26,012 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 26,012.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 26,013 - 38,628.

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
480	13523	28405	4.57				
860	13945	28603	10.48				
1046	14092		3.88				
1305	14341	27305	7.19				
1518	14650	27629	4.21				
1542	14674	27647	6.05				
1738	14788	27763	2.88				
1784	14793	27778	1.27				
1770	14798	27785	9.04				
1808	14832	27828	1.24				
1865	15016	28023	2.44				
2175	15191	--	2.92				
2287	15300	28324	2.97				
3200	16265	29776	3.13				
3494	16510	29431	1.32				
3527	16573	29460	10.05				
3574	16519		0.85				
3668	17008		1.15				
4225	17254	30141	1.66				
4290	17318	30186	6.25				
4310	17339	30218	0.63				
4310	17339	30218	0.83				
4364	17351		1.03				
4420	17447	30338	0.63				
4674	17691	30760	1.27				
4939	17674	30865	0.74				
5083	18083	30969	5.95				
5085	18105	30980	1.42				
5329	18435	31187	1.78				
5329	18435	31188	1.78				
5496	18536		4.07				
5678	18773		7.77				
5782	18868		3.49				
5824	18914	32087	0.85				

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5830	18320	32103	3.19				
6138	25655	32443	1.58				
6167	19242	32473	2.11				
6558	19616		1.24				
6700	19757	33034	0.89				
6700	19757	33035	0.89				
7332	20303	33647	1.52				
7332	20303	33648	1.52				
7642	20602	33966	1.45				
7642	20602	33967	1.45				
8114	21051		0.61				
8396	21365	34774	1.55				
8530	21787	35218	1.21				
9212	22178	35608	0.57				
9212	22178	35609	0.57				
9882	22845	36302	5.61				
10124	23050	36526	0.89				
10241	23166	36653	1.44				
10383	23305	36782	0.91				
10675	23597	37093	0.49				
10675	23597	37094	0.49				
10784	23715	37216	0.6				
10784	23715	37217	0.6				
11043	24007		2.14				
11366	24314		1.61				
11687	24653	38232	1.82				
11829	24712		1.94				
12888	25476	31730	1.34				
6170	18245	32477	15.3	9.9E+00	AJ293028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
8339	21308	34723	1.75	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
10100	23026	36502	0.47	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
10100	23026	36503	0.47	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
7184	20218	33549	0.66	9.8E+00	AF065630.1	NT	Cellulose synthase (OTC) gene, exon 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7184	20218	33550	0.66	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10787	23708	37209	1.19	9.0E+00	AF242432.1	NT	Mus musculus Nalp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalp1) and general transcription factor IIB polypeptide 2 (Gt2h2) genes, complete cds
10787	23708	37210	1.19	9.0E+00	AF242432.1	NT	Mus musculus Nalp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalp1) and general transcription factor IIB polypeptide 2 (Gt2h2) genes, complete cds
2835	15963	28913	3.21	9.4E+00	AB043785.1	NT	Mus musculus A13 gene for antithrombin, complete cds
6457	19822	32773	0.54	9.4E+00	P75130	SWISSPROT	HYPOPHOSPHATE-INDUCIBLE PROTEIN MG447 HOMOLOG
11911	24792	38381	2.45	9.4E+00	C69825	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
11911	24792	38382	2.45	9.4E+00	C69825	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
8435	21404	34817	0.86	9.3E+00	AF130590.1	NT	Human sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
9356	22321	35748	3.15	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5368	18474	31345	2.66	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5368	18474	31347	2.66	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9755	22726	31347	0.95	9.0E+00	P09241	SWISSPROT	RHODOPSIN
6152	19227	32456	5.62	8.9E+00	BE971806.1	EST_HUMAN	60165103871 NIH_MGC 31 Homo sapiens cDNA clone IMAGE:3934562 3'
6517	19560	32937	2.21	8.7E+00	AB019788.1	NT	Cynops pyrogastrus GpTox3 premature mRNA, partial cds
6517	19560	32938	2.21	8.7E+00	AB019788.1	NT	Cynops pyrogastrus GpTox3 premature mRNA, partial cds
440	13514	28445	1.03	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9810	21133	34538	3.58	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11504	24448		1.54	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8491	21459		0.82	7.6E+00	Z21459.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7568	20332		2.17	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8704	21872	35095	1.58	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8704	21872	35096	1.58	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5898	16885	32176	3.53	7.4E+00	BF700517.1	EST_HUMAN	602128878FT NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4285506 5'
9106	22072	35498	2.72	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
9106	22072	35498	2.72	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2890	16048	28968	4.7	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
2890	16048	28969	4.7	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
7230	20232	33559	1.12	7.2E+00	BE179030.1	EST_HUMAN	RC0-H10613-200306-031-e07 HT0613 Homo sapiens cDNA
7356	20236	33673	1.1	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7356	20236	33674	1.1	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9957	22884		6.96	7.1E+00	AL181565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11716	24678	38256	2.96	7.1E+00	P05850	SWISSPROT	HYPOTHEICAL 17.3 KDA PROTEIN IN MRD-PHPB INTERGENIC REGION
11909	24780	38379	4.81	7.1E+00	P06106	SWISSPROT	O-ACETYL SERINE SULFHYDRYLASE (OAS SULFHYDRYLASE)
10341	23256	38744	3.43	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
10341	23256	38744	3.43	7.0E+00	P48610	SWISSPROT	WD-40 REPEAT PROTEIN MS3
8626	21594	35014	3.94	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10716	23638	37131	1.32	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10734	23668	37149	0.44	6.9E+00	P34226	SWISSPROT	SKT5 PROTEIN
8240	21209	34613	1.31	6.8E+00	W03412.1	EST_HUMAN	z807c11.1 Scores melanocyte 2NBM Homo sapiens cDNA clone IMAGE:281860 5'
8240	21209	34613	1.31	6.8E+00	W03412.1	EST_HUMAN	z807c11.1 Scores melanocyte 2NBM Homo sapiens cDNA clone IMAGE:281860 5'
9488	22452		1.35	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS:
10569	23461	36983	3.31	6.8E+00	Q03670	SWISSPROT	OUTER CAPSID PROTEIN VP5 AND VP8]
5356	18461		0.74	6.6E+00	Q96028	SWISSPROT	HYPOTHEICAL 167.0 KDA PROTEIN C86C10.5 IN CHROMOSOME III
6695	19762	33029	0.72	6.6E+00	BF672121.1	EST_HUMAN	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
10434	23356	36842	1.87	6.6E+00	Q9Z507	SWISSPROT	602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293427 5'
10434	23356	36843	1.87	6.6E+00	Q9Z507	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11463	24406		2.49	6.6E+00	Q10308	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE CEC3.05G
9635	22488	35946	7.17	6.5E+00	P03374	SWISSPROT	ENY POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP38]
10667	23589	37096	0.47	6.5E+00	BE866001.1	EST_HUMAN	ENY POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP38]
10096	23025	36501	1.17	6.2E+00	AY010801.1	NT	Schizaphyllum commune unknown mRNA
10927	23847	37682	0.55	6.2E+00	6754821	NT	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
7298	23257	33591	1.35	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
10175	23100	36590	0.46	6.0E+00	AP000008.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt, position (617)
10880	23800	37302	0.63	6.0E+00	AEC001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10880	23800	37303	0.63	6.0E+00	AEC001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6670	19727	33003	6.7	5.9E+00	AF185142.1	NT	Mus musculus mixed lineage kinase 3 (Mick3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
3536	16682		0.88	5.9E+00	7661567	NT	Homo sapiens DESCT1 protein (DESC1), mRNA
7359	20339	33690	0.65	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor (gSR mRNA, complete cds
7369	20339	33691	0.66	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor (gSR mRNA, complete cds
7919	20788		1.5	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11905	23960	37485	2.98	5.6E+00	Q55276	SWISSPROT	LYOPENIN BETA CYCLASE

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6380	19448	32689	0.78	5.6E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10738	23064	37462	0.47	5.5E+00	P13963	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
11803	23958	37462	2.35	5.5E+00	P11960	SWISSPROT	PNEUMOLYSIN (THIO-ACTIVATED CYTOLYSIN)
7115	20049	33351	1.1	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7115	20049	33352	0.81	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7562	20515	34460	0.84	5.4E+00	Q96435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8143	21080	34460	0.8	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
8202	21172		1.72	5.4E+00	Q91062	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) (CONTAINS: LIPOVITELIN LV-1N; LIPOVITELIN LV-1C;
9151	22117	35543	0.73	5.4E+00	P40379	SWISSPROT	LIPOVITELIN LV-2)
9151	22117	35544	0.73	5.4E+00	P40379	SWISSPROT	REPI PROTEIN
10396	23318	36790	1.41	5.4E+00	Q17064	SWISSPROT	REPI PROTEIN
10396	23318	36800	1.41	5.4E+00	Q17064	SWISSPROT	RHODOPSIN
4824	17841	30739	1.22	5.3E+00	L43126.1	NT	RHODOPSIN
6635	16693		0.6	5.3E+00	P41779	SWISSPROT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
8415	21384		3.6	5.3E+00	P54098	SWISSPROT	HOMEOBOX PROTEIN CEH-20
9335	22300		0.53	5.3E+00	AB034090.1	NT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
11950	24829	38425	1.84	5.3E+00	Q27805	SWISSPROT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
12093	24964	38559	2.34	5.3E+00	Z77263.1	NT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
12093	24964	38560	2.34	5.3E+00	Z77263.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL141w
5539	18336		1.22	5.2E+00	BE184940.1	EST_HUMAN	S.cerevisiae chromosome VII reading frame ORF YGL141w
10738	23660		0.78	5.2E+00	AF248070.1	NT	QV4-H10691-Z/0400-188-109 H10591 Homo sapiens cDNA
11527	24468		1.48	5.2E+00	Q10138	SWISSPROT	Drosophila ommatidia RUB retrotransposable element reverse transcriptase gene, partial cds
9213	22278	35709	0.85	5.1E+00	Q16005	SWISSPROT	HYPOPHYSICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME I
10184	23109	36592	1.07	5.1E+00	P05192	SWISSPROT	RHODOPSIN
11617	24555	38117	3.01	5.1E+00	P55200	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
6418	19485	32734	0.65	5.0E+00	BF310443.1	EST_HUMAN	ZINC FINGER PROTEIN HRX (ALL-1)
10564	23476	37219	0.85	5.0E+00	BF306561.1	EST_HUMAN	601804010F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114.5'
10796	23717	38122	0.79	5.0E+00	AF182446.2	NT	601804020F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131909.5'
11622	24560		6.39	5.0E+00	Z83960.1	NT	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds
							Mycobacterium tuberculosis H37Rv complete genome, segment 103/162
							Human hereditary hemochromatosis region, histone 2A-like protein gene, hereditary hemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10562	23514		0.63	4.9E+00	U91328.1	NT	Eunice australis histone H3 (H3) gene, partial cds
40980	17124		9.81	4.8E+00	AF185295.1	NT	

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8494	21462	34878	0.53	4.8E+00	BF367808.1	EST_HUMAN	RC3, GN0042:100800-011-c10, GN0042 Homo sapiens cDNA
8896	21852		5.16	4.8E+00	AW750087.1	EST_HUMAN	PMD-B1047-3/10100-002-004 BT0847 Homo sapiens cDNA
289	13384	28311	2.03	4.7E+00	BF240552.1	EST_HUMAN	901875654F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4099716 5'
290	13384	28311	1.98	4.7E+00	BF240552.1	EST_HUMAN	901875654F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4099716 5'
3287	19341	29260	1.66	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8054	21001	34397	0.55	4.8E+00	U875989.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
9551	22513	35963	1.12	4.8E+00	BE646437.1	EST_HUMAN	7e95g10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292088 3' similar to TR:075140 075140
9551	22513	35964	1.12	4.8E+00	BE646437.1	EST_HUMAN	KIAA00646 PROTEIN, contains element PTRS repetitive element:
10755	23877		0.8	4.8E+00	AF240788.1	NT	KIAA00645 PROTEIN, contains element PTRS repetitive element:
8047	20984		0.81	4.8E+00	AF128177.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11930	24811	38409	2.19	4.5E+00	AE001044.1	NT	Ischaeferia orientalis isochlorophosphorylase synthase (PC1) gene, complete cds
12055	24928	38526	1.87	4.5E+00	BF698841.1	EST_HUMAN	Archaeoglobus fulgidus section 93 of 172 of the complete genome
3053	16110	29024	0.78	4.4E+00	BF530893.1	EST_HUMAN	902123238F1 NCL_CGAP_59 Homo sapiens cDNA clone IMAGE:4280216 5'
3053	16110	29025	0.76	4.4E+00	BF530893.1	EST_HUMAN	902123238F1 NCL_CGAP_59 Homo sapiens cDNA clone IMAGE:4280216 5'
6326	19396		1.89	4.4E+00	X13414.1	NT	602072585F1 NCL_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215284 5'
6394	19462	32709	0.59	4.4E+00	AF156696.1	NT	Murine I gene for MHC class II(a) associated invariant chain
6240	19313		0.71	4.3E+00	AF559878.1	NT	Nicotiana tabacum inorganic phosphate transporter (PT1) mRNA, complete cds
7672	20830	33864	3.53	4.3E+00	Y13402.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7672	20830	33864	3.53	4.3E+00	Y13402.1	NT	Pleurodinium falciparum R2382-var1 gene, exon 1
11210	24164	37694	7.01	4.3E+00	AF240788.1	NT	Tripterygium pallidum section 38 of 87 of the complete genome
11279	24230		1.83	4.3E+00	115268311	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5595	18691		3.57	4.2E+00	P16444	SWISSPROT	Homo sapiens Dipeptidyl aminopeptidase (DAP) gene, complete cds
5975	18770	31942	1.35	4.2E+00	P51826	SWISSPROT	Microsomal dipeptidase precursor (MDP) (DEHYDROPEPTIDASE-4) (RENAL DIPEPTIDASE) (RDP)
5954	18945		0.56	4.2E+00	O27630	SWISSPROT	LAF4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
8928	20162	33463	1.69	4.2E+00	P13983	SWISSPROT	PUTATIVE ATP-DEPENDENT HELICASE MTH802
8928	20162	33464	1.69	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9311	22278	35708	5.1	4.2E+00	A1809013.1	EST_HUMAN	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
10278	23203	36888	1.1	4.2E+00	P13368	SWISSPROT	wf87g03.x1 Source: NCL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2360892 3'
10508	23430		0.53	4.2E+00	P40898	SWISSPROT	NUBIN PROTEIN (TYANIN PROTEIN) (FOU DOMAIN PROTEIN 1) (PDM-1) (DFOU-19) (DOCT1)
							HEXOSE TRANSPORTER HXT8



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6046	25652	32334	0.84	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
6046	25652	32335	0.84	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
7319	20290	33633	0.76	4.1E+00	BE233868.1	EST_HUMAN	601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351634 5'
7420	20387	33738	0.55	4.1E+00	BF247939.1	EST_HUMAN	601165030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4069758 5'
7623	20868	34254	2.87	4.1E+00	O23810	SWISSPROT	Y11 PROTEIN PRECURSOR
8051	20868		0.84	4.1E+00	AB041523.1	NT	Pain-inducible vesicular mRNA for calcitonin A, complete cds
8065	21002	34398	3.95	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8065	21002	34399	3.95	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8249	21218	34628	2.5	4.1E+00	U37503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
8898	22651	36310	0.52	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
10031	22658	36428	2.43	4.1E+00	BF652425.1	EST_HUMAN	602247688F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
10669	23591		0.45	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
10981	23901	37414	0.47	4.1E+00	O84242	SWISSPROT	3-OXOACYL-ACYL-CARRIER-PROTEIN[SYNTHASE III] (BETA-KETOACYL-ACP SYNTHASE III) (KAS III)
11231	24184		2.3	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLF1
11317	24287		13.22	4.1E+00	BE85880.1	EST_HUMAN	601607510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3606051 5'
3556	16602		0.7	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5534	20057	33381	0.94	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5534	20057	33382	0.94	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7123	20057	33361	1.01	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7123	20057	33362	1.01	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7395	20363	33715	1.47	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
9225	22191	35621	0.44	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KIA0144
10303	23228	36711	0.43	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (NNOS)
10526	23446	36946	0.6	4.0E+00	AE002132.1	NT	Uraptasma iraei/uraptasma section 33 of 58 of the complete genome
10620	23542	37041	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10620	23542	37042	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11902	23957	37481	1.67	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11875	24757	38340	2.88	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11875	24737	38341	2.68	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS (NS1, NS2A, NS2B, NS4A AND NS4B); HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5); Nucleocapsid protein gene 50 for class I chikungunya
3513	16558	29483	4.65	3.9E+00	X64518.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
4349	17376		0.96	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5741	18835	32015	2.98	3.9E+00	BE814357.1	EST_HUMAN	MRQ-BN0070-300500-028-105 BN0070 Homo sapiens cDNA
5741	18835	32016	2.98	3.9E+00	BE814357.1	EST_HUMAN	MRQ-BN0070-300500-028-105 BN0070 Homo sapiens cDNA
6791	19845	33129	0.95	3.9E+00	AF288208.1	NT	Dicystatium discoidium non-L-TR retrotransposon TRES-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6848	19901	33195	0.67	3.9E+00	U61328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H2A-H) gene, Rofat gene, and sodium phosphate transporter (NPT3) gene, complete cds
7057	20079	33388	4.24	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
7587	20548	33908	4.15	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8660	21628	35049	2.34	3.9E+00	X65895.1	NT	Xlaevia mRNA for M4 muscarinic receptor
11720	23917	37434	2.83	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
11742	24827	38208	1.89	3.9E+00	AA681488.1	EST_HUMAN	h1812.1 NCL CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10418
2637	16536		1.27	3.8E+00	AE01562.1	NT	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN); Helicobacter pylori, strain 168 section 123 of 132 of the complete genome
6530	19593	32954	0.93	3.9E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
6937	20161	33482	0.59	3.8E+00	AI493849.1	EST_HUMAN	q251807.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030437 3'
8775	21742	35164	1.03	3.8E+00	D4725.1	EST_HUMAN	HUMSUPY135 Homo sapiens cDNA clone IMAGE:2030437 3'
10154	23079		0.99	3.8E+00	AJ390961.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7884
12118	24989		15.21	3.8E+00	9631284	NT	Metaphis sanguinea entomopoxvirus, complete genome
4049	17086	26982	9.75	3.7E+00	AL161539.2	NT	Anabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7372	20342		0.9	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
9058	22022		0.49	3.7E+00	4503950	NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
9532	22495	35943	0.92	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11760	24688	38269	1.73	3.7E+00	BF699279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11760	24688	38270	1.73	3.7E+00	BF699279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
12256	25082		2.8	3.7E+00	AB013746.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
595	13662	26575	4.04	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5286	12922	31153	0.63	3.6E+00	Z86109.1	NT	Bacillus subtilis complete genome (section 8 of 21): from 995501 to 1209940
5327	18433	31185	0.73	3.6E+00	BF316316.1	EST_HUMAN	U01001806F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4131018 5'
8897	21863	35285	0.93	3.6E+00	D12367.1	EST_HUMAN	H000007B08 Liver HepG2 cell line. Homo sapiens cDNA clone t808
8897	21863	35286	0.93	3.6E+00	D12367.1	EST_HUMAN	H000007B08 Liver HepG2 cell line. Homo sapiens cDNA clone t808
8892	21958	35393	4.21	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 528 of the complete genome
8892	21958	35394	4.21	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 528 of the complete genome
10022	22849	36416	0.44	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial, gene encoding mitochondrial protein, partial cds
10022	22849	36417	0.44	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial, gene encoding mitochondrial protein, partial cds
11200	24155		3.18	3.6E+00	M96795.1	NT	Escherichia coli glyceraldehyde 3-phosphate dehydrogenase (gldP) gene, partial cds, and the translation start site has been verified (gldP), the translation start site has been verified (gldP), and repressor protein (gldR) genes, complete cds
6115	19193		1.1	3.5E+00	L42898.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6337	19405	32847	0.96	3.5E+00	R19745.1	EST_HUMAN	X640208.1 Scans infant brain 1N1B Homo sapiens cDNA clone IMAGE:34940 5'
8087	21023	34422	0.5	3.5E+00	P97608	SW/SSPROT	5-OXOPROLINASE (5-OXO-L-PROLINASE)(PYROGLUTAMINASE)(5-OPASE)
8094	21030	34428	0.54	3.5E+00	AA692102.1	EST_HUMAN	037110.a1 Scans, testis, NHT Homo sapiens cDNA clone IMAGE:1618987 3' similar to gb:J04213
8124	21061	34459	0.56	3.5E+00	4505264	NT	CELLULAR RETINALDEHYDE-BINDING PROTEIN (HUMAN);
8629	21706		0.6	3.5E+00	P24557	SW/SSPROT	Homo sapiens macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (MST1R) mRNA
9387	22352	35762	0.91	3.5E+00	AA190998.1	EST_HUMAN	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
9387	22352	35763	0.91	3.5E+00	AA190998.1	EST_HUMAN	z86804.s1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains AUI repetitive element, contains element MSR1 repetitive element;
9850	22786	36240	0.96	3.5E+00	AL161553.2	NT	z86804.s1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains AUI repetitive element, contains element MSR1 repetitive element;
1514	14546	27517	5.3	3.4E+00	AF254577.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53
6893	19945	33241	0.49	3.4E+00	U77617.1	NT	Brassica napus RPBS5 mRNA, complete cds
7586	20547	33907	2.99	3.4E+00	P04052	SW/SSPROT	Chlorate-Aster yellow phytoplastid acetate kinase gene, complete cds
7968	20507	34298	0.9	3.4E+00	P04052	SW/SSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
9025	21991		0.88	3.4E+00	U65408.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNU1) gene, complete cds
9428	22392	35831	0.73	3.4E+00	AJ23042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
9487	22341	35889	0.95	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM5F2 gene for tetraspanin protein, exon 6
10627	23549	37049	2.59	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11861	24743	38327	2.86	3.4E+00	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
6186	19261	32496	1.03	3.3E+00	Q08669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6186	19261	32497	1.03	3.3E+00	Q08669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
8225	21194	34091	0.9	3.3E+00	AF11168.2	NT	Homo sapiens serine peptidyl transferase, subunit II gene, complete cds, and unknown genes
10830	23751	37250	0.9	3.3E+00	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5714
10830	23751	37251	0.9	3.3E+00	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5714
501	13573	28495	1.85	3.2E+00	X95422.1	NT	D. rerio zp-50 POU gene
4056	13573	28495	0.89	3.2E+00	X95422.1	NT	D. rerio zp-50 POU gene
4759	17776	30674	1.35	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5648	18744	31810	1.2	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5648	18744	31811	1.2	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5683	18776	31950	2.78	3.2E+00	P12763	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5683	18776	31951	2.78	3.2E+00	P12763	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6439	19504	32754	1.66	3.2E+00	P18631	SWISSPROT	NADH-LIBUQUINONE OXIDOREDUCTASE CHAIN 4
6439	19504	32755	1.66	3.2E+00	P18631	SWISSPROT	NADH-LIBUQUINONE OXIDOREDUCTASE CHAIN 4
7853	20807	34185	0.71	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
8052	20889	34385	2.47	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for psa9, ycf4, ycf4, ycf3, psa18 genes
8052	20889	34387	2.47	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for psa9, ycf4, ycf4, ycf3, psa18 genes
9385	22350	36298	4.78	3.2E+00	P13061	SWISSPROT	PERILASMIN [NIFE] HYDROGENASE SMALL SUBUNIT [NIFE HYDROGENYLASE SMALL CHAIN]
9888	22841	36298	1.87	3.2E+00	M35383.1	NT	S. cerevisiae threonine deaminase (ILDV1) gene, complete cds
10500	23422	36621	2	3.2E+00	AB016081.2	NT	Sus scrofa choline acetyltransferase gene, promoter region
12171	25055	36621	2.84	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5975	19060	32261	2.25	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7618	20578	33941	0.9	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)
7999	20838	34804	1	3.1E+00	AF303226.1	NT	Bacillus distalophilus pectate lyase (pelE) gene, complete cds
8424	21193	33538	0.43	3.1E+00	P40985	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
8949	21915	33538	4.37	3.1E+00	P40984	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE-1 IODEIODINASE) (DIOI) (TYPE 1 DII) (5D1)
8949	21915	33538	4.37	3.1E+00	P40984	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE-1 IODEIODINASE) (DIOI) (TYPE 1 DII) (5D1)
9614	22618		3.9	3.1E+00	Q14657	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL-D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9890	22833	36089	0.48	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
10256	23181	36638	0.86	3.1E+00	7524759	NT	Ginkgo biloba chloroplast, complete genome
10347	23271		0.61	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 56.3 KD PROTEIN F22C8.5 IN CHROMOSOME III

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10700	23622	37118	5.2	3.1E+00	P49365	SWISSPROT	DEOXYRIBOSYL SYNTHASE (DHS)
11781	23946		1.96	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11811	24696		2.76	3.1E+00	S66880.1	NT	retinoid acid nuclear receptor isoform beta 2 [intc, embryonal carcinoma cell line, PCCT-MZ1, mRNA, 2971 nt]
2849	15909	28533	1.5	3.0E+00	8923964	NT	Homo sapiens hypodermal protein PRO0889 (PRO0889), mRNA
5411	18514	31392	1.33	3.0E+00	X53066.1	NT	S aureus genes encoding Sau981 DNA methyltransferase and Sau861 restriction endonuclease
6708	19764	33043	0.78	3.0E+00	X58037.1	NT	Corynebacterium glutamicum thc gene for threonine synthase [EC 4.2.98.2]
6708	19764	33044	0.79	3.0E+00	X58037.1	NT	Corynebacterium glutamicum thc gene for threonine synthase [EC 4.2.98.2]
7383	20333		0.66	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH81)
7402	20370		0.59	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
9258	22224		1.21	3.0E+00	X67858.1	NT	B. rapae DNA for myosinase
10657	23579	37076	0.54	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
11008	23973	37497	1.65	3.0E+00	Q16181	SWISSPROT	COX10 PROTEIN HOMOLOG
11351	24301	37827	4.64	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F; RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE 2) (GC-F)
11351	24301						RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F; RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE 2) (GC-F)
11351	24301	37828	4.64	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F; RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE 2) (GC-F)
2026	15046	28059	2.33	2.9E+00	AE02225.2	NT	Chlamydia pneumoniae AR39, section 65 of 94 of the complete genome
6192	19266		0.6	2.9E+00	AB026033.1	NT	Bonapartia pediculus mitochondrial DNA for 16S ribosomal RNA
7084	20028	33332	1.97	2.9E+00	X38879.1	NT	P-primgit gdpapA gene for P-protein of the glycine cleavage system
7418	20385	33734	6.15	2.9E+00	Q14614	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7418	20385	33735	5.15	2.9E+00	Q14614	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7689	20647	34011	5.32	2.9E+00	P46569	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
8200	21170	34580	0.61	2.9E+00	P08644	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; MINOR STRUCTURAL PROTEIN VP3]
8200	21170						STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; MINOR STRUCTURAL PROTEIN VP3]
8434	21403	34616	0.82	2.9E+00	BF344171.1	EST_HUMAN	NONSTRUCTURAL PROTEIN VP4; CGAP_Bmt54 Homo sapiens cDNA clone IMAGE:4153059 5'
1451	14484	27460	4.16	2.9E+00	AF186338.1	NT	Buxus harlandii maltase K (mark) gene, partial cds, chloroplast gene for chloroplast product

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Single Exon Probes Expressed In Bone Marrow

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1637	14669		2.57	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7529	20492	33854	4.93	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
9072	22869		0.56	2.8E+00	BE566182.1	EST_HUMAN	601342756F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3984807 5'
11048	20492	33854	1.73	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
233	13333	26256	13.36	2.7E+00	6678308	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
233	13333	26257	13.36	2.7E+00	6678308	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
5631	18727	31888	1.11	2.7E+00	L14005.1	NT	Homo sapiens apoa polymorphism Kringle IV gene, exons 1 and 2
8485	21453		0.66	2.7E+00	U15947.1	NT	bonboa purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
9319	22284		1.69	2.7E+00	AL116459.1	NT	Batrachoseps chiroia strain T4 cDNA library under conditions of nitrogen deprivation
9787	21110	34510	0.64	2.7E+00	AW088191.1	EST_HUMAN	xc88872.x1 NCI_CGAP_Bn35 Homo sapiens cDNA clone IMAGE:2691374 3' similar to gb:U17733
10966	23766		1.69	2.7E+00	BE03527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4701	17722	30615	6.28	2.6E+00	AF086749.1	NT	CMD-BT0281-031199-087.H04 BT0281 Homo sapiens cDNA
5627	18723	31884	2.06	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5627	18723	31884	2.06	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5925	19011		3.9	2.6E+00	Y17052.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7803	26002		0.7	2.6E+00	AJ224639.1	NT	Mycobacterium fortuitum furA II gene
7967	20806		32.15	2.6E+00	AF235502.1	NT	Homo sapiens Surf-5 and Surf-9 genes
8394	21363	34770	1.12	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing insulin 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
8394	21363	34771	1.12	2.6E+00	AJ132180.1	NT	fabd bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
10015	22642	36408	3.12	2.6E+00	AL161540.2	NT	fabd bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
10720	23642		1.61	2.6E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
12841	25877		2.98	2.6E+00	11419220	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
1460	14493	27486	3.73	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1460	14493	27487	3.73	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5911	18997	32187	2.32	2.5E+00	P13485	SWISSPROT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5911	18997	32187	2.32	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6001	18987	32186	1.49	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6001	18987	32187	1.49	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6802	19844	33240	0.66	2.5E+00	D30052.1	NT	Vibrio cholerae cbaA gene and cbaB gene for cholera toxins, complete cds
7960	20801	34283	0.55	2.5E+00	P17588	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
8035	20572	34366	0.97	2.5E+00	AW040158.1	EST_HUMAN	LYT-RELATED PROTEIN 1
8095	21031	34429	0.51	2.5E+00	4502602	NT	QV4-FT0006-110500-205-007 FT0005 Homo sapiens cDNA
							Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9459	22423	35861	1.49	2.5E+00	D56307.1	NT	Rice DNA for adipsase C-1, complete cds
10211	23136	36623	0.73	2.5E+00	BE287788.1	EST_HUMAN	001175779F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5'
12214	25053		2.5	2.5E+00	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3028	16083	29006	1.1	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4944	17560	30551	5.31	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
6126	18204	32427	3.62	2.4E+00	P02843	SWISSPROT	VITELLOGENIN1 PRECURSOR (YOLK PROTEIN 1)
7806	20567	33927	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120866F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
7806	20567	33928	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120866F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
8479	21448	34984	2.08	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8479	21448	34985	2.08	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8554	21522		2.92	2.4E+00	AE001466.1	NT	Helicobacter pylori, strain J99, section 47 of 132 of the complete genome
8998	21964		1.46	2.4E+00	AW875126.1	EST_HUMAN	RC2:P10004:031269-011-005 P10004 Homo sapiens cDNA
9180	22146	35573	9.52	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
10398	23320	36803	2.34	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10398	23320	36804	2.34	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10498	23388	36882	2.1	2.4E+00	X92511.1	NT	H.sapiens CTGF gene and promoter region
10604	23528		6.1	2.4E+00	P09099	SWISSPROT	XYLULOSE KINASE (XYLULOKINASE)
10685	23607	37100	1.87	2.4E+00	BE326702.1	EST_HUMAN	h031063.x1 NC1 CGAP_K411 Homo sapiens cDNA clone IMAGE:3133187 3'
10685	23607	37101	1.87	2.4E+00	BE326702.1	EST_HUMAN	h031063.x1 NC1 CGAP_K411 Homo sapiens cDNA clone IMAGE:3133187 3'
10955	23875	37369	1.14	2.4E+00	O51481	SWISSPROT	DETERIFICATION REGULATORY PROTEIN NIRO
11415	24359	37694	2.2	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPKO operon and downstream
11517	24468		1.66	2.4E+00	AF066872.1	NT	Capra hircus alphaS2-casein type C gene, Intron 16
11686	24652	38231	2.14	2.4E+00	AF159652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1258	14263	27257	11.33	2.3E+00	Z46724.1	NT	G. domesticus artificial single chain antibody gene (L3)
4147	17178		1.45	2.3E+00	AIJ01081.1	NT	Bos taurus partial cys gene for cyclochrome b
5934	19020		0.96	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to
7687	20645	34009	2.42	2.3E+00	6978554	NT	PROLYL-CARBOXYPEPTIDASE
7653	20603		2.78	2.3E+00	P07199	SWISSPROT	Rattus norvegicus ATPase, Oar+ transporting, ubiquitous (Atp2a3), mRNA
8059	20996	34392	1.12	2.3E+00	X60285.1	NT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
9465	22429	35698	0.54	2.3E+00	5938317	NT	M. musculus and dros. genes homologues coding for DnaK and DnaJ
9525	22488	35936	2.03	2.3E+00	Q11127	SWISSPROT	Polyomus malpais mitochondrion, complete genome
							ALPHA(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)





Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10413	23335	38819	1.57	2.2E+00	AI290373.1	EST_HUMAN	q169b03.x1 Soares, placenta, 86cweeks. 2N6HFB29W Homo sapiens cDNA clone IMAGE:1893665 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10413	23335	38820	1.57	2.2E+00	AI290373.1	EST_HUMAN	q169b03.x1 Soares, placenta, 86cweeks. 2N6HFB29W Homo sapiens cDNA clone IMAGE:1893665 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10456	23378	36871	2.22	2.2E+00	BF246782.1	EST_HUMAN	q169b03.x1 Soares, placenta, 86cweeks. 2N6HFB29W Homo sapiens cDNA clone IMAGE:1893665 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10822	23743	37244	3.03	2.2E+00	AF183416.1	NT	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
11768	23923	37442	3.23	2.2E+00	P07811	SWISSPROT	Homo sapiens ovarian granulosa cell 13.0 kDa protein NSR74 homolog mRNA, complete cds
11937	24818	38415	6.31	2.2E+00	P10407	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
571	16944	26555	12.39	2.1E+00	AF132612.2	NT	EARLY E1A 28 KD PROTEIN
3601	16946		0.83	2.1E+00	AW448366.1	EST_HUMAN	U1H-B13-alk-e-08-Q1.1st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6253	19328		0.86	2.1E+00	P75357	SWISSPROT	HYPOPHYSICAL PROTEIN MS302 HOMOLOG
6980	20203	33532	3.45	2.1E+00	O70169	SWISSPROT	ALPHA-2-HS GLYCOPROTEIN PRECURSOR (FETUIN-A)
7225	20247	33581	0.61	2.1E+00	4503430	NT	Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
7246	19881	32278	5.97	2.1E+00	N29575.1	EST_HUMAN	W09a10.01 Soares, melanocytes 2N6HIM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654
8842	21809		1.82	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
1201	14240	27197	1.39	2.0E+00	AF180527.1	NT	AUT23630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5'
1201	14240	27198	1.39	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1339	14372	27342	1.19	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1573	14511		3.42	2.0E+00	P25582	SWISSPROT	Oryctolagus cuniculus Nsr-K-A1Pase beta 1 subunit mRNA, complete cds
2159	15176	28195	4.98	2.0E+00	Z78278.1	NT	PLATELET RNA METHYLTRANSFERASE SPB1
2159	15176	28196	4.98	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4127	17160	30048	2.24	2.0E+00	AW684496.1	EST_HUMAN	R.norvegicus mRNA for collagen alpha1 type I
4127	17160	30049	2.24	2.0E+00	AW684496.1	EST_HUMAN	HL3005.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
7798	20750		0.85	2.0E+00	P07566	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8358	21327	34738	3.84	2.0E+00	AB008678.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8358	21327	34739	3.84	2.0E+00	AB008678.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8358	21327	34740	3.84	2.0E+00	AB008676.1	NT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
8274	22240	35688	3.22	2.0E+00	F31500.1	EST_HUMAN	Escherichia coli 0157 DNA, map position at 48 min., complete cds
12756	25838	31427	4.52	2.0E+00	5834843	NT	Escherichia coli 0157 DNA, map position at 48 min., complete cds
							Escherichia coli 0157 DNA, map position at 48 min., complete cds
							HSPD222703 HMG Homo sapiens cDNA clone s4000117808
							Galus gallus mitochondrion, complete genome

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4820	17846	30748	0.98	1.8E+00	AF209468.1	NT	Danio rerio R550-like protein mRNA, complete cds
5679	18774	31946	4.52	1.8E+00	6754389	NT	Mus musculus Inositol 1,4,5-trisphosphate receptor 1 (Itp1), mRNA
5979	18774	31946	4.52	1.8E+00	6754389	NT	Mus musculus Inositol 1,4,5-trisphosphate receptor 1 (Itp1), mRNA
6219	19293	32527	1.05	1.9E+00	BE669695.1	EST_HUMAN	601897838F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 6'
5810	19864		1.19	1.9E+00	AW845888.1	EST_HUMAN	MRO-CT0069-07.059-002-002 CT0063 Homo sapiens cDNA
5912	19904		2.37	1.9E+00	Q63027	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN R44
8802	21798	35183	1.72	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8802	21769	35194	1.72	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8006	21972		3.6	1.9E+00	BF360206.1	EST_HUMAN	CM3-AT0114-010500-323-112 MT0114 Homo sapiens cDNA
9245	22211		1.52	1.9E+00	OS1781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
9988	22815	36380	0.53	1.9E+00	AA689125.1	EST_HUMAN	ab9404.x1 Strausgene lung (#837210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element/contains element L1 repetitive element ;
10929	23849	37364	0.83	1.9E+00	AF249289.1	NT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3109	16196	29077	1.5	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3137	16194	29103	10.81	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3137	16194	29104	10.81	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5967	19052		1.84	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6224	19298	32532	2.2	1.8E+00	BF315669.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6538	19600		1.19	1.8E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4238272 5'
6904	19908	33253	1.02	1.8E+00	BF305582.1	EST_HUMAN	601893488F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4136038 5'
7260	19995	33262	1.07	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
7476	20442		0.7	1.8E+00	P27127	SWISSPROT	LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE-GLUCOSYL) LIPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE
8454	21423	34638	0.9	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8454	21423	34639	0.9	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8812	21779	35204	0.46	1.8E+00	P46834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8812	21779	35205	0.46	1.8E+00	P46834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8812	21779	35206	0.46	1.8E+00	P46834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9206	22172	35803	2.21	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9530	22493	35941	0.66	1.8E+00	R31042.1	EST_HUMAN	YNT208.r1 Sceres placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9617	22561	36009	0.84	1.8E+00	AW680004.1	EST_HUMAN	QV0-OT0030-070300-148-403 OT0030 Homo sapiens cDNA
10208	23133	36620	0.93	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10616	23568		2.88	1.8E+00	AF111846.1	NT	Homo sapiens PRO0530 mRNA, complete cds
10919	23839		0.75	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12563	25608		8.17	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12642	25326		5.63	1.8E+00	9506402	NT	Rattus norvegicus Actin-related protein complex 1b (Arp1b), mRNA
1110	14154	27104	2.43	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2279	15292	28317	3.08	1.7E+00	AL183280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2382	15390	28415	1.67	1.7E+00	A1141067.1	EST_HUMAN	ø43903.X1 Soares, NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4487	17512	30400	0.9	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5694	18789	31959	1.66	1.7E+00	BE063546.1	EST_HUMAN	GMA-BT0282-171299-127-403 BT0282 Homo sapiens cDNA
5694	18789	31960	1.66	1.7E+00	BE063546.1	EST_HUMAN	GMA-BT0282-171299-127-403 BT0282 Homo sapiens cDNA
5955	19040	32238	0.49	1.7E+00	R58748.1	EST_HUMAN	G4846 Fetal heart Homo sapiens cDNA clone G4846 5' end
6133	19210	32436	3.14	1.7E+00	Q91TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1)
6703	19759	33038	0.59	1.7E+00	P35816	SWISSPROT	[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPC)
7428	20395	33746	1.01	1.7E+00	Q03703	SWISSPROT	HYPOPHETICAL 38.0 KD PROTEIN IN CAT2-AMDI INTERGENIC REGION
7428	20395	33747	1.01	1.7E+00	Q03703	SWISSPROT	HYPOPHETICAL 38.0 KD PROTEIN IN CAT2-AMDI INTERGENIC REGION
8187	21157	34566	0.81	1.7E+00	AF021335.1	NT	Mus musculus T-cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8367	21336	34746	1.21	1.7E+00	6755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (TAL1), mRNA
8397	21368	34775	0.54	1.7E+00	BF530330.1	EST_HUMAN	602071917F1 NCJ CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4214669 5'
8887	21853	35273	0.45	1.7E+00	AF245513.1	NT	Hippocampus hippocampus interferon inducible Mx protein (Mx) mRNA, complete cds
8974	21940		1.92	1.7E+00	BF308000.1	EST_HUMAN	G01894255F1 NIH JMG, 17 Homo sapiens cDNA clone IMAGE:4214669 5'
9052	22018	35442	0.51	1.7E+00	X69063.1	NT	M.musculus Aric-1 mRNA for erythroid enkyrin
9052	22018	35443	0.51	1.7E+00	X69063.1	NT	M.musculus Aric-1 mRNA for erythroid enkyrin
9168	22132	35556	0.43	1.7E+00	U19832.1	NT	Rattus norvegicus SA gene, partial cds
9504	25697	35909	2.37	1.7E+00	Q60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9504	25697	35910	2.37	1.7E+00	Q60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9965	22892		1.4	1.7E+00	AF161380.1	NT	Homo sapiens HSPC282 mRNA, partial cds
10332	23454		0.5	1.7E+00	AW953681.1	EST_HUMAN	EST365751 MAGE resequences, MAGE Homo sapiens cDNA

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## Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12518	25249	31803	1.78	1.7E+00	A1678443.1	EST_HUMAN	tu82d07.x1 NCI_OGAP_Qas4 Homo sapiens cDNA clone IMAGE:2287649 3' similar to contains MSR1.1t
2049	15098	28088	14.89	1.6E+00	AF199339.1	NT	MSR1 repetitive element.
2059	15078	28097	3.29	1.6E+00	AF077374.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2065	15033	28102	1.62	1.6E+00	Y11344.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2292	15304		1.33	1.6E+00	X98373.1	NT	Mus musculus ST6GanAcIII gene, exon 2
2972	16030	28953	1.88	1.6E+00	W58428.1	EST_HUMAN	B napus gene encoding endo-polygalacturonase
4063	17096		7.07	1.6E+00	BF570077.1	EST_HUMAN	z42610.1.1 Soares, Jetal, Jetal, NHH19W Homo sapiens cDNA clone IMAGE:341689 6' similar to
4378	17407	30287	1.29	1.6E+00	AF155827.1	NT	hpcD28805 N-ACETYL-LACTOSAMINE SYNTHASE (HUMAN)
4379	17407	30288	1.29	1.6E+00	AF155827.1	NT	602186055T1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4310591 3'
5120	18130	31006	2.98	1.6E+00	Y11344.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5120	18130	31007	2.98	1.6E+00	Y11344.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5928	18012	32204	2.21	1.6E+00	L04808.1	NT	Mus musculus ST6GanAcIII gene, exon 2
6020	19103	32305	0.82	1.6E+00	AF005831.1	EST_HUMAN	Brachydanio rerio MHC class I DA-beta-2701 gene, 3' end
6614	18672	32850	0.83	1.6E+00	BF390753.1	EST_HUMAN	IL2-UT0073-0609900-145-E02 UT0073 Homo sapiens cDNA
6668	18921	33217	0.97	1.6E+00	AW294881.1	EST_HUMAN	U1-H-B12-ahr-b-04-04-U1.s1 NCI_OGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7458	20422	33777	2.47	1.6E+00	BE587267.1	EST_HUMAN	RCO-CT0415-200700-032-ct10 CT0415 Homo sapiens cDNA
8064	21333		1.1	1.6E+00	Q48378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
9251	22117	35547	0.9	1.6E+00	AJ287131.1	NT	Mus musculus SIL_MAP_17, CYP_a, SCL & CYP_b genes
9251	22217	35547	0.9	1.6E+00	AJ287131.1	NT	Homo sapiens hypothetical protein PRO0671 (PRO0671), mRNA
9251	22217	35548	0.9	1.6E+00	X52048.1	NT	Homo sapiens hypothetical protein PRO0671 (PRO0671), mRNA
9815	25695	34540	1.54	1.6E+00	X52048.1	NT	Mus musculus COL3A1 gene for collagen alpha-1
9845	22872		0.48	1.6E+00	AF043468.1	EST_HUMAN	Mus musculus COL3A1 gene for collagen alpha-1
10091	23017	35493	1.23	1.6E+00	T41260.1	EST_HUMAN	Thermotoga bacteriophage D-xylose-binding protein (xyf) gene, complete cds
10508	23428	38925	0.48	1.6E+00	AF121361.1	NT	ph866_19/1TV Outward Alu-priated hrcDNA library Homo sapiens cDNA clone ph866_19/1TV
10545	23467	38931	1.12	1.6E+00	AW835544.1	EST_HUMAN	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase 1a (IAL), and
10545	23467	38932	1.12	1.6E+00	AW835544.1	EST_HUMAN	zinc finger protein (DNZ1) genes, complete cds
10709	23631	37126	0.78	1.6E+00	AF037352.1	NT	QVAL-T0016-060200-100-407 L'0016 Homo sapiens cDNA
11123	24083	37609	1.73	1.6E+00	F64817	SWISSPROT	QVAL-T0016-060200-100-407 L'0016 Homo sapiens cDNA
11192	19103	32305	5.78	1.6E+00	AF005831.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
12017	24994	38491	2.83	1.6E+00	AF104313.1	NT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
							Homo sapiens transglutaminase type 1 (Tgase1) gene, promoter region
							Homo sapiens unknown mRNA

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35	13156	28056	3.54	1.5E+00	U93449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
234	13334	28238	2.63	1.5E+00	AE002201.2	NT	Chlamydia pneumoniae AR39, section 32 of 94 of the complete genome
622	13687		2.04	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (melargidin) (Adam15), mRNA
2420	15427	28450	3.2	1.5E+00	AJ131402.1	NT	Ptdo virus A RNA complete genome, isolate U
2522	15526	28547	2.17	1.5E+00	6878390	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3155	15427	28450	2.96	1.5E+00	AJ131402.1	NT	Ptdo virus A RNA complete genome, isolate U
3386	16435	28382	0.82	1.5E+00	AE001945.1	NT	Dendrocybus radiorum R1 section 32 of 229 of the complete chromosome 1
5817	18907	32090	0.82	1.5E+00	AI655301.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237
5817	18907	32091	0.82	1.5E+00	AI655301.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237
6546	18607	32859	2.71	1.5E+00	R17879.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:31693 5'
7335	20306		1.48	1.5E+00	BE785356.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:3381555 5'
7368	20338	33688	16.72	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR
7568	20531	33690	0.6	1.5E+00	AA880259.1	EST_HUMAN	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR
7850	20796	34172	0.73	1.5E+00	AU003254.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1407115 3'
8144	21081		0.87	1.5E+00	AB039887.1	NT	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
8459	21426	34945	0.91	1.5E+00	BE897446.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
8514	21482	34896	0.48	1.5E+00	AB040887.1	NT	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
8991	21957	33382	1.08	1.5E+00	K02138.1	NT	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
9270	22335		0.47	1.5E+00	AB038516.1	NT	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
9489	22453	35893	0.95	1.5E+00	BF217818.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
9838	22774	36229	0.91	1.5E+00	R81928.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
9993	22820	36387	1.09	1.5E+00	AW375897.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
10219	23144		6.14	1.5E+00	BF376754.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
10412	23334		1.42	1.5E+00	BF337944.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
10556	23478	36972	2.82	1.5E+00	AA017889.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
10556	23478	36972	2.82	1.5E+00	AA017889.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
11727	24713	38190	5.98	1.5E+00	AL134187.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
11859	24751		6.39	1.5E+00	X07380.1	NT	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to
12112	24982	35893	1.53	1.5E+00	BE257552.1	EST_HUMAN	h12f10x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:1684893 3' similar to

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12382	28151		1.87	1.9E+00	5753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
12510	25809	31420	1.51	1.5E+00	D83480.1	NT	Human mRNA for KIA00746 gene, partial cds
12723	29376		4.94	1.5E+00	AL445055.1	NT	Thermoplasma acidophilum complete genome, segment 315
12821	25443		1.33	1.9E+00	6978492	NT	Rattus norvegicus 5'-Lipoxygenase (Alox5), mRNA
32	13152	26052	1.41	1.4E+00	7681685	NT	Human sapiens DKFZP686M0122 protein (DKFZP686M0122), mRNA
32	13152	26053	1.41	1.4E+00	7681685	NT	Human sapiens DKFZP686M0122 protein (DKFZP686M0122), mRNA
2295	15288		0.9	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (gluA) gene, complete cds
2341	15351		8.77	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2677	15873	28663	1.93	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2784	15776	28794	2.75	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSS1 protein (WSS1) genes, complete cds
2784	15776	28795	2.75	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSS1 protein (WSS1) genes, complete cds
3345	16396		0.63	1.4E+00	5453733	NT	Human sapiens Mad4 homolog (MAD4) mRNA
4284	17313	30191	1.38	1.4E+00	AW900455.1	EST_HUMAN	QMG-NN1005-140300-286-H06 NN1005 Homo sapiens cDNA
4284	17313	30192	1.38	1.4E+00	AW900455.1	EST_HUMAN	QMG-NN1005-140300-286-H06 NN1005 Homo sapiens cDNA
4590	16144	28056	0.92	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome
4590	16144	28057	0.92	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome
4615	17636		1.71	1.4E+00	BF881547.1	EST_HUMAN	602169837.1 NIH MGC, 83 Homo sapiens cDNA clone IMAGE:4287656 5'
5448	18548	31481	1.58	1.4E+00	AW054976.1	EST_HUMAN	W45907.x1 NCL_CGAP_Par1 Homo sapiens cDNA clone IMAGE:2510460 3'
5606	18702		5.52	1.4E+00	AB032983.1	NT	Human sapiens mRNA for KIAA1157 protein, partial cds
6410	19478	32725	3.06	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6427	25986		4.2	1.4E+00	AB020712.1	NT	Human sapiens mRNA for KIAA0605 protein, complete cds
6552	19813	32875	2.65	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6552	19813	32876	2.65	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6781	19836	33119	0.96	1.4E+00	BE007870.1	EST_HUMAN	QV0-BN0148-050500-215-b11 BN0148 Homo sapiens cDNA
6781	19836	33120	0.96	1.4E+00	BE007870.1	EST_HUMAN	QV0-BN0148-050500-215-b11 BN0148 Homo sapiens cDNA
6906	20122	33436	0.86	1.4E+00	AW593057.1	EST_HUMAN	QV3-NN0008-300300-132-b12 NN0008 Homo sapiens cDNA
							Human sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7503	20468	33629	2.02	1.4E+00	AJ133269.1	NT	hcd3105.x1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2818873 3' similar to contains Alu repetitive element
7521	20464	33848	1.15	1.4E+00	AW467760.1	EST_HUMAN	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7592	20542	33901	0.58	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7592	20544	33905	0.58	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)

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7611	20571	33935	0.66	1.4E+00	Q88905	SWISSPROT	MINOR CAPSID PROTEIN L2
8678	21646		0.6	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9146	22112		4.6	1.4E+00	AJ271735.1	NT	Homo sapiens Xa pseudobubalsonal region; segment 1/2
9448	22413	35849	1.56	1.4E+00	R20459.1	EST_HUMAN	Y93712.11 Scars infant brain (NIB Homo sapiens cDNA clone IMAGE:34345 5'
9552	22514	35955	3.46	1.4E+00	BE064667.1	EST_HUMAN	RCY-BT0313-301289-012.65 BT0313 Homo sapiens cDNA
9587	22549	36000	0.45	1.4E+00	AF194844.1	NT	Scalopus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10568	23490	36692	0.89	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10613	23535	37032	0.69	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-281058-008-C04 HT0198 Homo sapiens cDNA
10613	23535	37033	0.69	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-281058-008-C04 HT0198 Homo sapiens cDNA
10892	23812	37319	0.92	1.4E+00	D63441.1	NT	Pandora clematis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10892	23812	37320	0.92	1.4E+00	D63441.1	NT	Pandora clematis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11559	24199	38055	4.43	1.4E+00	AB006882.1	NT	Homo sapiens APECD mRNA for AIRE-1, complete cds
11733	24619	38196	2.83	1.4E+00	BE982107.2	EST_HUMAN	601655184R1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3845805 3'
11733	24619	38197	2.83	1.4E+00	BE982107.2	EST_HUMAN	601655184R1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3845805 3'
11756	24684	38263	2.15	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (peg1) gene, complete cds
11756	24684	38264	2.15	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (peg1) gene, complete cds
12360	25627		1.7	1.4E+00	AL181500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
13068	25602		1.4	1.4E+00	7657624	NT	Homo sapiens atafin (Drosophila, RNA-binding protein) homolog 2 (STAU2), mRNA
572	13641		1.56	1.3E+00	Z73640.1	NT	Musculo gene encoding 4-dihydropyrimidin-5-ribose dehydrogenase
903	13958	28616	3.12	1.3E+00	AJ271182.1	NT	Cantharalis sp. partial 26S rRNA gene, isolate Tibet
1131	14174		32.4	1.3E+00	Y16213.1	NT	Homo sapiens putative psbHBA pseudogene for hair keratin, exons 2 to 7
1300	14336	27296	19.22	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (ZF157) mRNA
1300	14336	27300	19.22	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (ZF157) mRNA
1358	14393		0.89	1.3E+00	U61730.2	NT	Cob (acetylme-3d) dihydrodipicolinate synthase (dapA) gene, complete cds
1614	14646		2.59	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2255	15769		1.22	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPs and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2415	15422	28445	1.03	1.3E+00	P25391	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2557	15560		2.8	1.3E+00	BE96735.2	EST_HUMAN	601661238R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915645 3'
2950	16007	28931	0.67	1.3E+00	8755821	NT	Mus musculus alpha-spectrin 1, erythro (Sptn1), mRNA

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3611	16656	29574	1.02	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), prolidase C-proteinase enhancer protein (PCLCE) genes, complete c>
5264	18290	31152	0.9	1.3E+00	AJ390500.1	NT	Candida albicans partial mRNA for ribonucleotide reductase large subunit (rrf1 gene)
5592	18688	31657	1.08	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5794	18888	32067	0.52	1.3E+00	M27198.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
6063	19144	32355	0.54	1.3E+00	BF66825.1	EST_HUMAN	802146264F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309095 5'
6134	19211	32437	8.25	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0285-291169-004-408 CT0289 Homo sapiens cDNA
6134	19211	32438	8.25	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0285-291169-004-408 CT0289 Homo sapiens cDNA
6557	19617	32882	1.14	1.3E+00	M33496.1	NT	D melanogaster roco-transient A gene product, complete cds
6914	19866		0.89	1.3E+00	Q00159	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6956	20181		0.54	1.3E+00	P49940	SWISSPROT	SPORE GERMINATION PROTEIN KB
7014	20140	33457	0.81	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
7124	25673	33363	0.52	1.3E+00	AW821890.1	EST_HUMAN	IL2-ST0311-020200-040-G12 ST0311 Homo sapiens cDNA
7141	20117	33430	1.04	1.3E+00	BE638819.1	EST_HUMAN	601091420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5'
7307	20278	33616	0.8	1.3E+00	BE243571.1	EST_HUMAN	TC9AP1D0969 Pediatric pre-B cell acute lymphoblastic leukemia B-cell-HGSC project=TC9A Homo sapiens cDNA clone TC9AP0969
7691	20649	34013	0.72	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8041	21009	35032	1.09	1.3E+00	AJ008912.1	NT	Sus scrofa pig gene
8790	21767	35179	2.29	1.3E+00	BE96379.2	EST_HUMAN	601657145R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868185 3'
8907	21873	35299	0.87	1.3E+00	BE974280.1	EST_HUMAN	601660250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3860632 3'
9059	22025		1.88	1.3E+00	9810247	NT	Homo sapiens GL004 protein (GL004), mRNA
9142	22108	35534	0.92	1.3E+00	A1827629.1	EST_HUMAN	w05507.x1 NC1_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2462100 3'
9873	22326		4.88	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/sulfotransferase-2 gene, complete cds
9962	22835	36288	2.2	1.3E+00	X72019.1	NT	S. alba p1r-1 mRNA for photolase
9982	22935	36289	2.2	1.3E+00	X72019.1	NT	S. alba p1r-1 mRNA for photolase
9982	22909	36374	1.02	1.3E+00	AF059250.1	NT	Homo sapiens ALPHA-MANNOSIDASE (ALOX12B) mRNA, complete cds
10029	22968	36424	1.57	1.3E+00	Q00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
10108	23034	36511	1.32	1.3E+00	A1827629.1	EST_HUMAN	w05507.x1 NC1_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2462100 3'
10185	23110	36593	0.83	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-1147 chromosomal inversion junction DNA
10185	23110	36594	0.83	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-1147 chromosomal inversion junction DNA
10225	23150	36639	3.75	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868185 3'



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10266	23211		0.64	1.3E+00	AI55944.1	EST_HUMAN	ttg7a12.x1 NCI CGAP_UH Homo sapiens cDNA clone IMAGE:2214814 3' similar to gp.X14723
10509	23431	36927	0.45	1.3E+00	AF061251.1	NT	CLUSTERIN PRECURSOR (HUMAN); Escherichia coli serotype O157:H7 O antigen gene cluster
10509	23431	36928	0.45	1.3E+00	AF061251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10574	23466	39899	1.24	1.3E+00	AE004392.1	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
10591	23513	37006	1.53	1.3E+00	M23953.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10948	23868		0.85	1.3E+00	AL163302.2	NT	Homo sapiens chromosome 21, segment HS21C102
10975	23895	37409	0.49	1.3E+00	AI660946.1	EST_HUMAN	ws32a10.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2468922 3' similar to SW-TRXB_HUMAN
10987	23907		0.43	1.3E+00	8623637	NT	Q16881 THIOREDOXIN REDUCTASE ;
11052	24015		3.63	1.3E+00	Q14117	SWISSPROT	Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA
11252	24203	37727	2.35	1.3E+00	P25239	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTONINASE) (DHP)
11273	24225	37751	1.71	1.3E+00	Z16892.2	NT	MRNA 3'-END PROCESSING PROTEIN RNA15
11867	24749	38331	2.61	1.3E+00	Z42042.1	NT	Bacillus subtilis desmin gene
11945	24825	38420	2.1	1.3E+00	Z96692.1	NT	Human mRNA for KIAA0083 gene, partial cds
12001	24878		1.55	1.3E+00	Z1891.1	NT	Arabidopsis thaliana 3-ketacyl-acyl carrier protein synthase II (KAS II) mRNA, complete cds
12468	25239		3.37	1.3E+00	AF187873.1	NT	602023185.F1 NCI CGAP_B067 Homo sapiens cDNA clone IMAGE:4158452 5'
12669	25344	31762	0.47	1.3E+00	BF346043.1	EST_HUMAN	ET1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12679	25724		3.24	1.3E+00	P33464	SWISSPROT	Slutaria illum cytochrome b gene, complete cds, mitochondrial gene for mitochondrial product
12765	25407		1.68	1.3E+00	AF187035.1	NT	Z122408.s1 Soares_fetal_liver_spleen_1NLS.S1 Homo sapiens cDNA clone IMAGE:431535 3'
651	13717	26639	13.29	1.2E+00	AA676246.1	EST_HUMAN	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
824	13982	26833	1.37	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
824	13982	26834	1.37	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
824	13982	26835	1.37	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
879	13934		0.95	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1165	14206	27160	7.4	1.2E+00	AF080245.2	NT	Ellele's oleiferia sesquiterpene synthase mRNA, complete cds
1210	14248	27206	1.43	1.2E+00	AL252242.1	NT	pes seed-borne mosaic virus complete genome
1210	14248	27207	1.43	1.2E+00	AL252242.1	NT	pes seed-borne mosaic virus complete genome
2025	16045	28068	1.06	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3127	16184	29093	0.99	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3179	16234	29151	8.14	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3179	16234	29152	8.14	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3296	16352		3.07	1.2E+00	PF4910	SWISSPROT	CONUGAL TRANSFER PROTEIN TRBE PRECURSOR
3367	16417	29343	0.78	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3725	16767	29678	8.46	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (Pc7) gene, exons 1 to 6, partial cds
4012	17051	29857	1.76	1.2E+00	BF373570.1	EST_HUMAN	MR0-F10175-050900-203-g08.1 F10175 Homo sapiens cDNA
4327	16417	29343	1.08	1.2E+00	AF198740.1	NT	Homo sapiens LHX3 gene, intron 2
4498	17523		2.12	1.2E+00	M87080.1	NT	Rattus reticus cardiac AEG gene, exons 1-23
4551	17574	30464	1.33	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4592	17613	30507	2.1	1.2E+00	AF156465.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4619	17640		0.6	1.2E+00	Y06200.1	NT	T. plantum chloroplast tbc1 gene, partial
5052	18064	30942	2.38	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5052	18064	30943	2.36	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5052	18064	30944	2.36	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5512	18612	31544	1.06	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5634	18730	31892	1.89	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 S10191 Homo sapiens cDNA
5894	18982		0.57	1.2E+00	X81876.1	NT	Calicivirus cDNA for orf1, orf2 and orf3
5874	19059	32260	0.78	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6275	19248	32580	2.39	1.2E+00	X74985.1	NT	D. hydei eyf repeat cluster DNA, fragment D
6339	19407	32648	4.12	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-r03 BN0090 Homo sapiens cDNA
6423	19480	32741	1.41	1.2E+00	X85084.1	NT	C. glutamicum pla gene and ackA gene
6423	19480	32742	1.41	1.2E+00	X85084.1	NT	C. glutamicum pla gene and ackA gene
6467	19532	32780	38.6	1.2E+00	AA759254.1	EST_HUMAN	enb1g12.s1 Soares, testis, NHT Homo sapiens cDNA clone 1322374.3'
6575	19635	32901					W39512.s1 Soares melanocyte ZNF-HM Homo sapiens cDNA clone IMAGE:273599.3 similar to gblm87955 HUMANALU472 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb:J04970
6550	19708	32984	0.71	1.2E+00	P17671	EST_HUMAN	CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6854	19711	32988	2.01	1.2E+00	AW813276.1	EST_HUMAN	ECDSONE-INDUCIBLE PROTEIN E75-A
7100	20034	33337	1.17	1.2E+00	AB028901.1	NT	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
7113	20047	33346	2.68	1.2E+00	AJ002141.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7465	20431		0.84	1.2E+00	AJ271735.1	NT	Mus musculus DSPP gene
7610	20685	33934	1.04	1.2E+00	AF734585.1	EST_HUMAN	Homo sapiens Xa pseudotubosomal region, segment 1/2
7612	20655	34243	2.6	1.2E+00	X74207.1	NT	AV734585 cDNA Homo sapiens cDNA clone cDNAAF03.5
8122	21069	34457	0.53	1.2E+00	BE787846.1	EST_HUMAN	Lactate pyD and pyF genes
8615	21881	35307	3.24	1.2E+00	AB033030.1	NT	G01481761F1 NIH_MGC_08 Homo sapiens cDNA clone IMAGE:3884270.5'
							Homo sapiens mRNA for KIAA1204 protein, partial cds
							ALPHA, ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE)
9010	21979	35396	0.85	1.2E+00	P38427	SWISSPROT	

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9229	22194		0.58	1.2E+00	7706271	NT	Homo sapiens CGI-30 protein (LOC51611), mRNA
9360	22345	35777	1.88	1.2E+00	AW377210.1	EST_HUMAN	MR2-C10222-201059-001-437 C10222 Homo sapiens cDNA
9364	22566	36006	0.47	1.2E+00	H48599.1	EST_HUMAN	yc9da06.f1 Soares fetal liver spleen 1N1FS Homo sapiens cDNA clone IMAGE:202068 5'
9753	22694	36150	3.63	1.2E+00	Z32850.1	NT	R commutis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9764	22891	36353	1.71	1.2E+00	D11745.1	EST_HUMAN	HUMHMTA01 Liver HepG2 cell line. Homo sapiens cDNA clone ntnt1601
10291	23216	36700	3.52	1.2E+00	X56332.1	NT	H.sapiens ENO3 gene for muscle specific endase
10589	23611		0.73	1.2E+00	AG009666.1	NT	Homo sapiens klotho gene, exon 1
11674	24640	38219	1.89	1.2E+00	AW817817.1	EST_HUMAN	PMAS-ST0264-167199-001-401 ST0264 Homo sapiens cDNA
11713	24676		7.68	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11785	23940	37462	2.59	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12466	25798	31524	18.09	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12487	25232		2.7	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 9/14
464	13537	29463	1.43	1.1E+00	D85890.1	NT	Human mRNA for KIAA0227 gene, partial cds
1777	14806	27762	1.97	1.1E+00	AW695393.1	EST_HUMAN	QYQ-BN0042-176300-163-412 BN0042 Homo sapiens cDNA
1915	14938	27935	1.08	1.1E+00	AW575989.1	EST_HUMAN	U1-HF-BRP-alk-F02-C-U1-1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'
3341	16392	23313	7.34	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3341	16392	23314	7.34	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3498	16345	23471	0.79	1.1E+00	882264.1	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3593	16638	29556	3.34	1.1E+00	AI808350.1	EST_HUMAN	W54H11.XT Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to
3731	16773	29584	1.52	1.1E+00	AE003886.1	NT	SW-PS31_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3731	16773	29585	1.52	1.1E+00	AE003886.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3831	16871		0.85	1.1E+00	X85374.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3864	17004	29918	0.87	1.1E+00	862264.1	NT	H.paraheмоphilicus hohIM(A), hohIM(G), hohIR and menB genes
4050	17087	29983	1.02	1.1E+00	6755205	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4243	17272		6.78	1.1E+00	5835331	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA
5028	18042	30925	3.15	1.1E+00	U18468.1	NT	R.unicornis complete mitochondrial genome
							African swine fever virus, complete genome
5085	18095	30971	3.91	1.1E+00	U34740.1	NT	Emmericella nidulans sterigmatocystin biosynthetic gene cluster: (stcA), (stcB), (stcC), (stcE), (stcF), (stcG), (stcH), (stcI), (stcJ), (stcK), (stcL), (stcM), (stcN), (stcO), (stcP), (stcQ), (stcR), (stcS), (stcT), (stcU), (stcV) and (stcW) genes, complete cds
5109	18119	30993	1.04	1.1E+00	X78425.1	NT	E.faecalis pbp5 gene
5269	18276	31139	0.9	1.1E+00	6830080	NT	Homo sapiens putative GR9 protein (GR9), mRNA
5380	18484	31359	1.93	1.1E+00	6878530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5695	18790	31961	13.39	1.1E+00	BE960184.1	EST_HUMAN	001652776RT NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825505 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5715	18909	31987	0.99	1.1E+00	AI135592.1	EST_HUMAN	q85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735250 3'
6211	19285	32517	1.03	1.1E+00	11419739	NT	Homo sapiens soluble carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6405	19473	32721	0.94	1.1E+00	AF197861.1	EST	Macroglypta pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6547	19608	32870	0.83	1.1E+00	RO6037.1	EST_HUMAN	ye8903.r1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone IMAGE:124924 5'
6876	19929	33226	1.21	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7468	20434		0.68	1.1E+00	AF101091.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 25 through 28
7514	20478	33840	0.82	1.1E+00	X55981.1	NT	Maze mRNA for endase (2-phospho-D-glycerate hydrolase)
7732	20687	34050	1.83	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7732	20687	34051	1.83	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7754	20707	34078	8.13	1.1E+00	AI161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7833	25691	34158	0.94	1.1E+00	11987980	NT	Mus musculus silent mating type information regulation 2, (S.cerevisiae, homolog)-like (Sir2), mRNA
8470	21439	34857	2.95	1.1E+00	BF693396.1	EST_HUMAN	602082562F1 NHT_MGC_81 Homo sapiens cDNA clone IMAGE:4246828 5'
8563	21531	34851	0.73	1.1E+00	AI478339.1	EST_HUMAN	tn39h11.x1 NCL_CGAP_K611 Homo sapiens cDNA clone IMAGE:2160549 3'
9089	22056	35479	0.63	1.1E+00	AB000388.1	NT	Acetabularia calciculus mitochondrial COXI-like gene
9167	22133	35559	1.42	1.1E+00	S80750.1	NT	YHant-vyomogovirus glycoprotein B antibody 4D4 heavy chain variable region [human], mRNA, partial, 375
9278	22244	35673	0.45	1.1E+00	AI079646.1	EST_HUMAN	cz34105.x1 Soares_NHMPV_S1 Homo sapiens cDNA clone IMAGE:1877249 3'
9792	21115		0.64	1.1E+00	BE344876.1	EST_HUMAN	601276279F1 NHT_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9898	22913	36378	0.95	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
10040	22967		0.69	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
10130	23016	36634	0.95	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
10192	23317	36601	1.39	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
10287	23222	36706	5.56	1.1E+00	AI161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10397	23281	36757	20.52	1.1E+00	6794021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10687	23787	37287	1.09	1.1E+00	P73789	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10889	23909	37422	0.63	1.1E+00	BF343944.1	EST_HUMAN	602014489F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150508 5'
10989	23909	37422	0.63	1.1E+00	BF343944.1	EST_HUMAN	602014489F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150508 5'
11012	23877	37502	2.03	1.1E+00		NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
11064	24027		3.83	1.1E+00	AF068942.1	NT	Klebsiellidium fulgens cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11435	18340		4.65	1.1E+00	8822673	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11439	24382	37921	3.12	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (c68PDH1) mRNA, complete cds
11439	24382	37922	3.12	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (c68PDH1) mRNA, complete cds
11683	24549	38227	3.44	1.1E+00	AB096989.1	EST_HUMAN	wf7e11.11 Soares, NEL T, GBC S1 Homo sapiens cDNA clone IMAGE:2381548.3
12439	25202		3.12	1.1E+00	P07068	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12539	25263	31807	1.55	1.1E+00	AF216966.1	NT	Taenia solium immunogenic protein 1578 mRNA, partial cds
12651	25706		2.26	1.1E+00	AF234169.1	NT	Dicystellum discoidium isopentenyl pyrophosphate isomerase (DipI) mRNA, complete cds
99	13215		1.55	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
113	13224	28148	1.56	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
418	13491		3.03	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA and 26S rRNA
578	13647	28560	2.22	1.0E+00	AJ251660.1	NT	Gliricidia ligaria mRNA for homeodomain transcription factor (ho gene)
678	13741	28688	6.74	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
679	13742		1.35	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1388	15066		3.53	1.0E+00	X80418.1	NT	V. carchariae Algal-GAM mRNA
1771	14800	27786	0.97	1.0E+00	AB008531.1	NT	Plasmodium falciparum RNA for nonstructural polyprotein, capsid precursor, complete cds
2493	15496	28521	1.42	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2493	15496	28522	1.42	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2887	15946	28861	4.42	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2887	15946	28862	4.42	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2978	16036		0.81	1.0E+00	O14226	SWISSPROT	HYPOPHOSPHATE 67.9 KD PROTEIN C8F12.08C IN CHROMOSOME I
3212	16287	29160	1.08	1.0E+00	AA029453.1	EST_HUMAN	429p08.51 Soares, total fetus, Nb2H8.9w Homo sapiens cDNA clone IMAGE:1032830.3 similar to
3613	13215		0.93	1.0E+00	U23808.1	NT	WP-C42D9.3 CE04204, contains element MER22 MER22 repetitive element;
3693	16736	29648	1.33	1.0E+00	AJ223816.1	NT	Xenopus laevis rhodopsin gene, complete cds
4097	17131	30024	1.16	1.0E+00	AF223391.1	NT	Agaricus bisporus mRNA for tyrosinase
4304	17333		0.73	1.0E+00	8822645	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4843	17860	30755	1.54	1.0E+00	AL163247.2	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5053	18065		0.9	1.0E+00	D10852.1	NT	Homo sapiens chromosome 21 segment HS21C047
							Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5554	18450	31328	3.23	1.0E+00	Z67022.1	NT	Hordium vulgare gene encoding cysteine proteinase
5949	19035	32228	5.05	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5949	19035	32228	5.05	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6067	19148	32800	1.44	1.0E+00	Z67341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA config fragment No. 6
6238	19308	32541	4.52	1.0E+00	P04501	SWISSPROT	FIBRIN PROTEIN
6243	19316	32648	1.77	1.0E+00	AW452782.1	EST_HUMAN	UHH-B18-48x-4-98-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068689 3'
6637	19695	32872	2.12	1.0E+00	U75902.1	NT	UHH-B18-48x-4-98-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068689 3'
6691	19748	33025	0.68	1.0E+00	AF104689.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6768	19841		0.98	1.0E+00	P46508	SWISSPROT	SREB-11 PROTEIN
6813	19887	33155	0.71	1.0E+00	BE767718.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6813	19887	33156	0.71	1.0E+00	BE767718.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6944	20188	33481	1.17	1.0E+00	Y11204.1	NT	V. carteri gene encoding vdxoxopain
7033	18365	31252	0.64	1.0E+00	U63721.1	NT	Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds
7345	20316	33661	1	1.0E+00	S52770.1	NT	Insulin-like growth factor-binding protein 4 (cathele, pulmonary artery endothelial cells, mRNA, 2028 nt)
7719	20676		8.7	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE)
7979	20918	34309	1.52	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7997	20936	34330	6.07	1.0E+00	AA775191.1	EST_HUMAN	602153702F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:8683781 3'
8165	21103		0.57	1.0E+00	BF676213.1	EST_HUMAN	602153702F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294727 5'
8294	21263	34673	1.49	1.0E+00	BE368267.1	EST_HUMAN	601443650F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3848005 5'
8294	21263	34674	1.49	1.0E+00	BE368267.1	EST_HUMAN	601443650F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3848005 5'
8481	18065		1.22	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
							PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE, D-3-HYDROXYACYL COA DEHYDROGENASE]
8693	21661	35084	2.31	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE, D-3-HYDROXYACYL COA DEHYDROGENASE]
8693	21661	35085	2.31	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE, D-3-HYDROXYACYL COA DEHYDROGENASE]
8821	21786		0.83	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBQUITIN THIOLESTERASE 11) (UBQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8855	21822	35242	0.44	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8855	21822	35243	0.44	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8883	22696		2.37	1.0E+00	BE147331.1	EST_HUMAN	RC1-H10229-181059-011+00 H10229 Homo sapiens cDNA
8923	21889	35316	0.89	1.0E+00	U42720.2	NT	Human immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
9075	22041	35484	1.55	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
9026	22570	36019	2.14	1.0E+00	BE907562.1	EST_HUMAN	Human immunodeficiency virus 70 Homo sapiens cDNA clone IMAGE:3869421 5'
9838	22772	36227	1.25	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9838	22772	36228	1.25	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9969	22896	36359	1.94	1.0E+00	AV88554.1	EST_HUMAN	AV88554 GK6 Homo sapiens cDNA clone KCQCYA11 5'
9974	22901	36364	1.23	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
9974	22901	36365	1.23	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
10212	23137	36624	0.56	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10212	23137	36625	0.56	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10471	23363	36839	0.72	1.0E+00	5174562	NT	Human Coronavirus gene for membrane protein
10471	23363	36840	0.72	1.0E+00	5174562	NT	Human Coronavirus gene for membrane protein
10564	23486	36980	0.68	1.0E+00	A077020.1	EST_HUMAN	Human sapiens MHC binding factor, beta (MHCBBF) mRNA
10564	23486	36980	0.68	1.0E+00	A077020.1	EST_HUMAN	Human sapiens MHC binding factor, beta (MHCBBF) mRNA
10690	23612	37106	3.7	1.0E+00	AV756825.1	EST_HUMAN	cyf16a07 at Scars, senescent, fibroblasts, NBHSF Homo sapiens cDNA clone BNFAC04 5'
10842	23762	37262	20.08	1.0E+00	AA004982.1	EST_HUMAN	AV756825 BM Homo sapiens cDNA clone BNFAC04 5'
10842	23762	37263	20.08	1.0E+00	AA004982.1	EST_HUMAN	AV756825 BM Homo sapiens cDNA clone BNFAC04 5'
10876	23768	37297	1.18	1.0E+00	U11910.1	NT	ZNF402.17 Soares, fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:426906 5'
12048	18459	31328	1.68	1.0E+00	Z97022.1	NT	ZNF402.17 Soares, fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:426906 5'
12327	25129		3.28	1.0E+00	P15306	SWISSPROT	Human telodendria susceptibility gene exon 1-27, complete cds
12327	25129		3.28	1.0E+00	P15306	SWISSPROT	Human telodendria susceptibility gene exon 1-27, complete cds
12650	25333		2.49	1.0E+00	AW97184.1	EST_HUMAN	Thordum vulgaris gene encoding cysteine protease
1575	14608	27590	3.22	9.0E-01	AF245455.1	NT	EST388265 MAGLE resequences, MAGN Homo sapiens cDNA
1575	14608	27591	3.22	9.0E-01	AF245455.1	NT	EST388265 MAGLE resequences, MAGN Homo sapiens cDNA
1575	14608	27581	3.22	9.0E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOO III mRNA, complete cds
2645	15642	28666	1.1	9.0E-01	AL163002.2	NT	Drosophila melanogaster regulator of G-protein signalling LOO III mRNA, complete cds
3619	19603		1.1	9.0E-01	AF14585.1	NT	Homo sapiens chromosome 21 segment HS21C102
3619	19603		1.1	9.0E-01	AF14585.1	NT	Homo sapiens chromosome 21 segment HS21C102
5717	18811	31360	8.82	9.0E-01	P49637	SWISSPROT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5717	18811	31360	8.82	9.0E-01	P49637	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5969	19054	32254	0.79	9.8E-01	Q06532	SWISSPROT	PROBABILE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
5916	22560		1.4	9.8E-01	U95887.1	NT	Lycopodium esculentum putative Mt1 copy 1 nematode-resistance gene
5913	22734		3.02	9.8E-01	Q28642	SWISSPROT	B2-BRADYKININ RECEPTOR (BK-2 RECEPTOR)
11068	24032	37556	1.48	9.8E-01	AJ005028.1	NT	Dmelo rero mRNA for Epi-like receptor tyrosine kinase rtk8
524	13595	26513	1.12	9.8E-01	P22587	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2305	14317		1.26	9.8E-01	AJ003108.1	NT	Callitrichi jacchus UBE1 gene derived retroposon on the Y chromosome
2813	15805		1.29	9.8E-01	AF174844.1	NT	Xenopus laevis rca GTPase mRNA, complete cds
7406	20374	33725	4.12	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JN983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JN983
7406	20374	33726	4.12	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JN983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JN983
7907	20850	34236	0.89	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE3860049 5'
7907	20850	34237	0.99	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE3860049 5'
9060	22035	35458	0.88	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10804	23725		0.53	9.8E-01	AA825565.1	EST_HUMAN	cd55604.s1 NCL CGAP_G08T Homo sapiens cDNA clone IMAGE1371847 3'
11339	24299	37813	2.06	9.8E-01	BE258705.1	EST_HUMAN	601110259F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE3350750 5'
11339	24280	37814	2.06	9.8E-01	BE258705.1	EST_HUMAN	601110259F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE3350750 5'
12545	25268		1.41	9.8E-01	U92111.2	NT	Homo sapiens X26 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein > end e, partial cds
7386	20336	33686	2.3	9.7E-01	U28716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d
8848	21815	35235	1.81	9.7E-01	AF14912.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8854	21821	35241	1.33	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (ret)
11505	24447		3.87	9.7E-01	BF511209.1	EST_HUMAN	U11-H-B14-and-e-07-U11 at NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE3308140 3'
12117	24987	38569	2.29	9.7E-01	U87514.1	NT	Deletostellum discoideum CAR3 gene, promoter region
4486	17511	30399	1.68	9.6E-01	AW789674.1	EST_HUMAN	PM2-UM0053-240300-005-12 UM0053 Homo sapiens cDNA
5179	19188	31065	0.9	9.6E-01	7862375	NT	Homo sapiens KIA00914 gene product (KIA00914), mRNA
5947	19937	32121	3.85	9.6E-01	Z70556.1	NT	Panovirus B19 DNA, patient C, genome position 2448-2894
5947	19937	32122	3.85	9.6E-01	Z70556.1	NT	Panovirus B19 DNA, patient C, genome position 2448-2894
8610	19962	33258	0.57	9.6E-01	Z87341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
8735	21703		1.21	9.6E-01	X86275.1	NT	P. falciparum complete gene map of plaiid-like DNA (IR-4)
9203	22169	35569	0.51	9.6E-01	U81138.1	NT	Rattus norvegicus (strain R41) Rps2r gene, complete cds



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9446	22410	35347				NT	Mus musculus WNT-2 gene, partial cds, putative ankyrin-related protein and cyclic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds, and unknown gene
11848	24731	38317	0.44	9.6E-01	AF228943.1	NT	AV752605 NFD Homo sapiens cDNA clone NPDBAG06 5'
11848	24731	38318	3.04	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NFD Homo sapiens cDNA clone NPDBAG06 5'
12223	25060		3.04	9.6E-01	AV752605.1	EST_HUMAN	Homo sapiens centrosomal protein 2 (C2P2), mRNA
12239	25060		2.19	9.6E-01	11421722	NT	Sphyrna liburo NADH dehydrogenase subunit 2 (NDH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
12839	25874	31416	3.03	9.6E-01	U91423.1	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
2484	15488	28512	1.03	9.5E-01	7705591	NT	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3796	18838	28741	2.39	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3796	18838	28742	2.39	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
6934	22319	35745	0.68	9.5E-01	AI190162.1	EST_HUMAN	q457607.XT Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9461	22425	35663	1.1	9.5E-01	AF951102.1	EST_HUMAN	RC1-CT0285-241189-011-002 CT0285 Homo sapiens cDNA
11574	24512	39069	1.5	9.5E-01	BE218711.1	EST_HUMAN	601885103F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103530 5'
11780	23935	37456	1.52	9.5E-01	AW250798.1	EST_HUMAN	UIH-B12-ethp-L03-ALU1a1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3214	16269		3.77	9.4E-01	AF163560.1	NT	Plimphella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
3231	16286		1.93	9.4E-01	AF080568.1	NT	Human Fe-gamma-receptor (FCGR2A) gene, exon 4
9217	22183	35616	0.69	9.4E-01	M90724.1	NT	Human Fe-gamma-receptor (FCGR2A) gene, exon 4
12460	25235		2.08	9.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3969929 5'
12638	25790					NT	Homo sapiens adenosine growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1745	14774		1.93	9.4E-01	11419857	NT	Homo sapiens phytoerythrin (PHYH) gene, exon 5
1745	14774		1.34	9.3E-01	AF242822.1	NT	RC5-BT0503-271189-011-801 BT0503 Homo sapiens cDNA
1741	15639	28663	1.01	9.3E-01	BE071172.1	EST_HUMAN	Bovine papillomavirus type 2, complete genome
4066	17102	29663	0.82	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4068	17102	29664	0.82	9.3E-01	M20219.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5673	18766	31940	1.47	9.3E-01	AF213884.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
5761	18854	32034	3.92	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7954	20517		0.76	9.3E-01	AF270648.1	NT	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8402	21371	34779	1.78	9.3E-01	AA847040.1	EST_HUMAN	cd08003.1 NCL CGAP_O2 Homo sapiens cDNA clone IMAGE:1356357
9165	22131		0.95	9.3E-01	AF061681.1	NT	Xenopus laevis CCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
9289	22295	35685	0.91	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12953	25528	31713	1.34	9.3E-01	11440288	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 2 (ITPR2), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12965	25534		3.29	9.2E-01	AF271207.1	NT	Adenosine triphosphatase putative large subunit ribosomal protein rpl34 mRNA, complete cds
3253	19307	20231	3.14	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3816184 3'
5908	18986		1.73	9.2E-01	7108410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
8101	19180	32399	4.04	9.2E-01	BF037586.1	EST_HUMAN	601481153F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3864661 5'
6789	19843	33127	0.51	9.2E-01	M64703.1	NT	N-acetylserine synthetase (cys-20/urc-3) gene
10018	22945	36412	0.77	9.2E-01	AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
10105	23031	36509	1.21	9.2E-01	6871677	NT	Mus musculus carbonic anhydrase 4 (Ca4), mRNA
10628	23550	37050	3.42	9.2E-01	11430663	NT	Homo sapiens yeast-like protein 1 (LALP1), mRNA
10780	23701	37189	1.84	9.2E-01	BF568351.1	EST_HUMAN	7658603.x1 NCI CGAP K1611 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SWNU5M_TRYBB
12031	24907	38501	1.54	9.2E-01	BF132402.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5:
1620	14892	27638	2.31	9.1E-01	T86675.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
2134	15151		2.08	9.1E-01	8923056	NT	ye52071.s1 Scarsa fetal liver spliced INFLS Homo sapiens cDNA clone IMAGE:121989 3' similar to contains Alu repetitive element;
2562	15583	28602	1.12	9.1E-01	AF062819.1	NT	Homo sapiens hypopharyngeal protein FLJ20048 (FLJ20048), mRNA
3218	16273	28195	1.11	9.1E-01	T28418.1	EST_HUMAN	Pseudomonas fluorescens DNA polymerase II (dnaE) gene, complete cds
3218	18273	29196	1.11	9.1E-01	T28418.1	EST_HUMAN	AB200068 Infant brain, L1NL array of Dr. M. Soares IN1B Homo sapiens cDNA clone LLAB200G8 5'
6291	19363	32602	1.88	9.1E-01	L36033.1	NT	AB200068 Infant brain, L1NL array of Dr. M. Soares IN1B Homo sapiens cDNA clone LLAB200G8 5'
6655	19712	32859	2.94	9.1E-01	Q81704	SWISSPROT	Human pre-B cell stimulating factor homologue (SDFlb) mRNA, complete cds
7827	20775	34152	18.4	9.1E-01	AA806623.1	EST_HUMAN	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (TIHEAVY CHAIN H3)
8011	20949	34342	2.58	9.1E-01	U72995.1	NT	cb71g98.s1 NCI CGAP G081 Homo sapiens cDNA clone IMAGE:1338862 3'
10536	23458	36935	0.45	9.1E-01	P38432	SWISSPROT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
12580	25867		10.31	9.1E-01	AF050113.1	NT	P80-COILIN
4408	17434	30319	1.77	9.0E-01	AF069810.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
7622	20582	33946	0.65	9.0E-01	L42547.1	NT	Homo sapiens neurokinin B gene, partial cds
7652	20812		1.32	9.0E-01	D38321.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
8704	22657	36112	0.55	9.0E-01	AF066761.1	NT	Xenopus laevis gene for aldolase, complete cds
10189	23114	36598	0.44	9.0E-01	U39702.1	NT	Danio rerio anemaphorin Z1a mRNA, complete cds
							Myoplasma genitalium section 24 of 51 of the complete genome
5781	18873	32054	2.37	8.9E-01	AF028198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
6577	19445		1.28	8.9E-01	X60986.1	NT	Rabbit MHC fragment RLA-DF DNA

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6605	25063	32937	0.69	8.9E-01	BF217939.1	EST_HUMAN	601682708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095218 5'
6605	25063	32938	0.69	8.9E-01	BF217939.1	EST_HUMAN	601682708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095218 5'
7408	20375		0.54	8.9E-01	AB042287.1	NT	Homo sapiens P15 gene for 6-pyruvyltetrahydropterin synthase, complete cds
8553	21521		0.43	8.9E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8769	21736	35157	1.09	8.9E-01	AF259667.1	NT	Chitonia nana cytochrome-c oxidase subunit 1 (cox1) gene, partial cds; mitochondrial gene for mitochondrial product
12074	24946	39541	2.99	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
12420	25190		5.46	8.9E-01	AE002189.2	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
4573	17095	30489	1.98	8.9E-01	O260390	SWISSPROT	POTATIVE F420-DEPENDENT NADP REDUCTASE
5238	18246		0.9	8.9E-01	L41654.1	NT	Trypanosoma brucei microtubule-associated protein (MAP15) mRNA, 3' end of cds
5447	18549	31462	0.7	8.9E-01	AF310817.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
11418	24362	37897	2.31	8.9E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
12082	24954	38549	6.51	8.9E-01	AA080055.1	EST_HUMAN	cc38H11.s1 NCL_CGAP_GC051 Homo sapiens cDNA clone IMAGE:1352037 3' similar to contains Alu repetitive element/transposon element MER22 repetitive element 1;
12237	23592	19538	2.73	8.9E-01	D90911.1	NT	Synchytriosis sp. PCO8803 complete genome, 13127, 1576593-1719843
465	13636	26464	1.8	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2411	15418	28442	0.91	8.7E-01	5901893	NT	Homo sapiens A1-binding transcription factor 1 (ATBF1), mRNA
2885	15944	28859	5.42	8.7E-01	AA593863.1	EST_HUMAN	indBff11.s1 NCL_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877
5043	18056		2.78	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa lipopolysaccharase (lpp), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
5247	18255	31125	0.97	8.7E-01	BF216308.1	EST_HUMAN	601683175F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095378 5'
8374	21343	34754	0.65	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-128500-013-c07 NN0057 Homo sapiens cDNA
9282	22248	35677	0.71	8.7E-01	AI239456.1	EST_HUMAN	qf35606.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1946788 3'
9282	22249	35678	0.71	8.7E-01	AI239456.1	EST_HUMAN	qf35606.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1946788 3'
10095	23021	36406	1.32	8.7E-01	AE004993.1	NT	Pseudomonas aeruginosa PAO1, section 524 of 529 of the complete genome
11181	24137	37669	4.56	8.7E-01	BF3683970.1	EST_HUMAN	GVG-NN1021-100900-337-c03 NN1021 Homo sapiens cDNA
12042	24917	38512	3.97	8.7E-01	BF107694.1	EST_HUMAN	6016823684RT NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
12042	24917	38513	3.97	8.7E-01	BF107694.1	EST_HUMAN	6016823684RT NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
475	13547		2.65	8.9E-01	X17012.1	NT	Rat IGf1 gene for insulin-like growth factor II
859	13915	28874	4.32	8.9E-01	W69089.1	EST_HUMAN	zid4403.r1 Soares_fetal_heart_NHH1019W Homo sapiens cDNA clone IMAGE:343516 5'
2278	15291	28316	1	8.9E-01	4503210	NT	Homo sapiens cyclochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthinohydrolase), polypeptide 1 (CYP27A1b) mRNA
3635	16878	26592	0.87	8.9E-01	AI181565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3813	18953	28760	1.38	8.6E-01	U49724.1	NT	Drosophila melanogaster melitin (Dmectin) mRNA, complete cds
5207	18216	31091	2.8	8.6E-01	BE147609.1	EST_HUMAN	CH1-HT0226-160300-019-c05 HT0228 Homo sapiens cDNA
6001	19084	32283	7.79	8.6E-01	X00547.1	NT	Chicken lipoprotein lipase gene
6001	19084	32284	7.79	8.6E-01	X00547.1	NT	Chicken lipoprotein lipase gene
6515	25661	32835	0.54	8.6E-01	S7872.1	NT	polyprotein [Coxsackie B4 virus CB4, host=mouse, E2, originally derived from Edwards CB4 human strain, genomic RNA, Complete, 7387 nt]
8887	18920	33215	1.7	8.6E-01	AF143732.1	NT	Gus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
9887	18920	33216	1.7	8.6E-01	AF143732.1	NT	Gus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7770	20723		0.81	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 strain 66 of 134 of the complete genome
8290	21229		1.29	8.6E-01	AF001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
8371	21346	34757	0.51	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapse response mediator protein (CRMP) mRNA, complete cds
10044	22971		0.48	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12788	25717		1.44	8.6E-01	AL112162.1	NT	Burkholderia strain T4 cDNA library under conditions of nitrogen deprivation
8888	19940	33235	1.5	8.5E-01	AF185214.1	NT	Bacteriophage D3, complete genome
7768	20721	34093	2.49	8.5E-01	BE542612.1	EST_HUMAN	801067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3493505 5'
8323	21292	34708	0.42	8.5E-01	AL161572.2	NT	Anabidopsis thaliana DNA chromosome 4, contig fragment No. 88
8761	21728	35150	0.83	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8761	21728	35151	0.93	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8849	21816	35236	0.57	8.5E-01	AJ248213.1	NT	Homo sapiens partial 5HT4 receptor gene, exons 2 to 5
10715	23637	37129	1.35	8.5E-01	AB008799.1	NT	Cyathium caldarium gene for SigC, complete cds
10715	23637	37130	1.35	8.5E-01	AB008799.1	NT	Cyathium caldarium gene for SigC, complete cds
12585	25869		2.25	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
12572	25883		1.37	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4782	17802	30683	0.85	8.4E-01	AF083975.2	NT	Pow adenovirus 8, complete genome
5571	25641	31627	2.68	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5571	25641	31628	2.68	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
8107	21044	34443	0.51	8.4E-01	AF051142.1	NT	Maneattia brassicae phenomene binding protein 2 precursor (PBP2) mRNA, complete cds
10317	23241		3.28	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
12005	24882	38478	1.54	8.4E-01	M55584.1	NT	Human collagenase type IV (CLG4) gene, exon 4
3111	19198	29078	3.01	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3111	19198	29078	3.01	8.3E-01	AL161506.2	NT	Anabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3823	15863	29767	0.83	8.3E-01	AB010879.1	NT	Nicotiana glauca mRNA for chloroplast ribosomal protein L10, complete cds
4040	17078	28978	3.16	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5341	18446	31199	2.42	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10028	22955		4.53	8.3E-01	AI791852.1	EST_HUMAN	nm011212 NC1 CGAP_C09 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR11 THR repetitive element;
10469	23591	36866	1.1	8.3E-01	AF036070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10579	23901	36993	3.97	8.3E-01	AF108133.1	NT	Mus musculus neuro-44 gene, exons 3 through 12 and partial cds
11033	23997	37524	2.97	8.3E-01	AEO00903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 149) of the complete genome
11050	24013		1.92	8.3E-01	Z712472	NT	Phytophthora infestans mitochondrion, complete genome
11634	24671	38136	2.22	8.3E-01	AF020503.1	NT	Homo sapiens FRAS3 common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
2068	15085	28103	2.24	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2101	15118		1.08	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tin) gene, complete cds
2688	15684		1.06	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
3918	16958	28871	0.75	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
3940	16980	29895	0.92	8.2E-01	AF063417.1	NT	Taraxacum officinale elongation factor 1-alpha mRNA, partial cds
6900	19854	33139	0.57	8.2E-01	X95283.1	NT	G.gallus mRNA for C-Serrat-1 protein
6900	19854	33140	0.57	8.2E-01	X95283.1	NT	G.gallus mRNA for C-Serrat-1 protein
6941	20165	33468	0.85	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SCIL25 protein
7082	20103	33474	3.69	8.2E-01	AW379433.1	EST_HUMAN	CM4-H10243-081196-037-e01 HT0243 Homo sapiens cDNA
7484	25682	33807	4.38	8.2E-01	Z12126.1	NT	S.cerevisiae MET, LEU4, and POL1 genes encoding MET14 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8787	21754	35176	0.58	8.2E-01	BE263145.1	EST_HUMAN	60114485F2 NH1_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
10385	23307	36785	0.66	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
10419	23341	36827	1.59	8.2E-01	AF052659.1	NT	Homo sapiens thiorodotin-related protein mRNA, complete cds
10963	23305	36968	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10963	23305	36969	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10751	23673	37169	3.84	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMANBARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10751	23673	37170	3.84	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMANBARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11957	24836	38432	2.97	8.2E-01	L10127.1	NT	Mollusca contagiosum virus type 1 ORF1 and ORF2 DNA
12038	24913	38507	4.82	8.2E-01	P10393	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
12043	24918	38514	6.1	8.2E-01	H87398.1	EST_HUMAN	yw144021.1 Soares, placenta, 865weeks, 2NH-PetabW Homo sapiens cDNA clone IMAGE:252195 5'
12586	25290	-31781	2.98	8.2E-01	AJ001261.1	NT	similar to gbmM39072 90S RIBOSOMAL PROTEIN L7A (HUMAN);
2769	15751		1.48	8.1E-01	AF191839.1	NT	Mus musculus mRNA for NIPSNAP2 protein
3472	16518	29439	3.67	8.1E-01	AF050605.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds

Table 4  
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3472	18518	29440	3.67	8.1E-01	AF055098.1	NT	Homo sapiens MHC class 1 region
5792	18884	32068	0.51	8.1E-01	Q01727	SWISSPROT	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR)
6448	18513	32763	0.84	8.1E-01	U16790.1	NT	Mus musculus putative collagen alpha-2 (Xl) chain (COL11A2) gene, partial cds
6777	18832	33114	2.47	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
6777	18832	33115	2.47	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
7755	20708	34077	0.95	8.1E-01	O47477	SWISSPROT	CYTOSOLIC CYTOCHROME B
8243	21212	34618	1.12	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picoat) gene, partial cds; putative sodium channel (Nacch) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gpr) gene, partial cds
8243	21212	34619	1.12	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picoat) gene, partial cds; putative sodium channel (Nacch) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gpr) gene, partial cds
8956	21922	35349	0.91	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8956	21922	35350	0.91	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
9122	22088	35516	1.13	8.1E-01	AW242647.1	EST_HUMAN	09e288 x1 NCI_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2692469 3' similar to SW1YAR_MOUSE
10484	23408	36902	0.84	8.1E-01	P08425	SWISSPROT	ONE288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN, contains MER22 b1 PTR5 repetitive element
10776	23697	37165	0.42	8.1E-01	N84541.1	EST_HUMAN	PROBABLE E4 PROTEIN
11812	24697	38277	4.05	8.1E-01	BE83558.1	EST_HUMAN	KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' similar to EST(LOCN C-0P'E11)
11812	24697	38278	4.05	8.1E-01	BE83558.1	EST_HUMAN	RC0-TN0080-220900-025-d10 TN0080 Homo sapiens cDNA
12298	25109	31639	1.73	8.1E-01	AE001711.1	NT	RC0-TN0080-220900-025-d10 TN0080 Homo sapiens cDNA
178	13278	178	3.32	8.0E-01	AJ271510.1	NT	Thermoboga maritima section 23 of 136 of the complete genome
288	13383	26310	5.97	8.0E-01	AJ132772.1	NT	Staphylococcus aureus partial pla gene for phosphate acyltransferase allele 15
2051	15070	26310	1.72	8.0E-01	BF530982.1	EST_HUMAN	Bos taurus tub and rtf genes
3083	16151	28085	1.41	8.0E-01	AF127697.1	NT	9020724731 NCI_OGAP_Brm97 Homo sapiens cDNA clone IMAGE:4215091 5'
3324	16376	28266	1.3	8.0E-01	AF0006183.1	NT	Salimiri boliviensis olfactory receptor (SBO27) gene, partial cds
3717	16760	28266	2.36	8.0E-01	AL162758.2	NT	Mus musculus gene for olfactory G-protein, complete cds
4563	17596	30478	6.45	8.0E-01	X83739.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7
8322	21231	35259	2.31	8.0E-01	AV901489.1	EST_HUMAN	G galactose 4-epimerase (GAL4) beta 3 subunit
8870	21837	35259	1.05	8.0E-01	Y11085.1	NT	RC0-TN1012-270300-021-h06 NN1012 Homo sapiens cDNA
11303	24253	37778	1.98	8.0E-01	Q92783	SWISSPROT	Rice stripe virus RNA 3
							CREB-BINDING PROTEIN

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
454	19327	26457	0.78	7.9E-01	D11478.1	NT	Lymnaea digastr nuclear polyhedrosis virus gene for DNA polymerase, complete cds
716	13778		0.78	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1606	14641		23.05	7.9E-01	AB040985.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1663	14695		1.28	7.9E-01	U32793.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2272	15295	28311	7.38	7.9E-01	AB004616.1	NT	Oryzctegus carinatus mRNA for mitsugumin29, complete cds
2273	15296	28312	2.36	7.9E-01	AF130459.1	NT	Danio rerio Tpt4-associated protein Tapr1A (tapr1A) mRNA, complete cds
3528	16574	29497	3	7.9E-01	AF228964.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4330	17358		0.88	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:3535785 5'
4842	17663	30551	1.15	7.9E-01	6753745	NT	Mus musculus embigin (Emb) mRNA
4842	17663	30552	1.15	7.9E-01	6753745	NT	Mus musculus embigin (Emb) mRNA
5244	18252	31123	1.03	7.9E-01	AF228943.1	NT	Mus musculus WINT-2 genes, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
6479	19544	32792	0.76	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8448	21415	34828	3.37	7.9E-01	X90965.1	NT	P.cadum GR gene
6905	22857	36319	4.3	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
10409	23331	36816	4.3	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10457	23373	36864	0.82	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GK6 Homo sapiens cDNA clone GKGDRE12 3'
10877	23797	37298	0.82	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTD9-4-keto-L-rhamnose reductase, complete cds
11350	24300		2.81	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072) mRNA
11546	24487	38041	2.22	7.9E-01	P16022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
877	13932		1.96	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1k104
2283	15298	28320	6.12	7.8E-01	AW859567.1	EST_HUMAN	ES1371637 MAGE sequences, MAGF Homo sapiens cDNA
4730	17790	30642	1.33	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5075	18065		0.8	7.8E-01	AW753353.1	EST_HUMAN	RC3-C10284-130100-023-c02 C10254 Homo sapiens cDNA
6187	19825	32498	2.5	7.8E-01	AF115856.1	NT	Sphenodon punctatus alpha endase mRNA, partial cds
6344	19413	32655	1.04	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6906	19694	32659	0.72	7.8E-01	JAL45068.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
8836	21893	35221	1.26	7.8E-01	BF106927.1	EST_HUMAN	71654005.x1 Soares NSF_F8_9W_01_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526178 3'
9369	22551	36002	1.34	7.8E-01	Y10759.1	NT	D discoidium recGAP gene
9697	22640	36097	0.52	7.8E-01	4826973	NT	Homo sapiens nucleoporin 214kD (NUP214), mRNA
10483	23405		1.01	7.8E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (NDL-ALPHA1)

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12559	25848		2.32	7.8E-01	L28280.1	NT	Arabidopsis thaliana 1-amino-1'-cyclopropanecarboxylate synthase (ACS6) gene, complete cds
145	13248	26177	6.69	7.7E-01	AF184346.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
727	13788		3.26	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (A2alpha) and major histocompatibility protein class II beta chain (Eb2a) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like
2724	15718	28736	2	7.7E-01	Q33915	SWISSPROT	CITRATE SYNTHASE
3368	16418		0.76	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactoseamine:polypeptide N-acetyl-galactosaminyltransferase 7 (GALNAc-T7) (GALNAc-T7), mRNA
3614	16658	29578	3.83	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4425	17452	30343	3.04	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4425	17452	30344	3.04	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5640	18736	31699	1.25	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5640	18736	31900	1.25	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6066	19147	32359	0.53	7.7E-01	R08600.1	EST_HUMAN	Y24602.31 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:127755 3'
10204	23129	36616	0.72	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12447	25207		5.53	7.7E-01	11457621	NT	Archaeoglobus fulgidus, complete genome
6218	10292	32525	4.49	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6218	19292	32526	4.49	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6687	19724	32969	0.65	7.6E-01	P37938	SWISSPROT	MATNG-TYPE PROTEIN A-ALPHA 24
7026	19361	31248	0.98	7.6E-01	AI253399.1	EST_HUMAN	ac14b12.1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030878
7026	19361	31252	0.98	7.6E-01	AI253399.1	EST_HUMAN	ac14b12.1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030878
7262	19987	33285	0.89	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-lactalbumin receptor mRNA, complete cds
8400	21369	34778	1.33	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhip (Tphip) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (PFT27) gene, complete cds; and HSAR (Hsar) gene, complete cds
8464	21433	34849	1.92	7.6E-01	6857762	NT	Mus musculus actin (Actin-pending), mRNA
8464	21433	34850	1.92	7.6E-01	6857762	NT	Mus musculus actin (Actin-pending), mRNA
8668	21636	35058	0.43	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NM2A) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NM2A2C)
8668	21636	35059	0.43	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NM2A) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NM2A2C)



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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9318	22283	35714	1.01	7.9E-01	6753577	NT	Mus musculus cytochrome P450, 29g, phenobarbital inducible, type a (Cyp2b9), mRNA
9634	22578	36028	5.25	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9634	22878	36028	5.25	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11085	24851	36229	2.09	7.6E-01	X96347.1	NT	H. aspersa mRNA for neurofilament NF70
11085	24851	36230	2.09	7.6E-01	X96347.1	NT	H. aspersa mRNA for neurofilament NF70
12020	24697		3.05	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
12203	25045		3.8	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
514	13985		1.97	7.3E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
586	13654	26598	1.01	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7764	20717	34090	0.78	7.6E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (ephr) mRNA, complete cds
12516	25247		4.53	7.5E-01	AF165151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
13027	25575	31697	1.57	7.6E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
1132	14175	27124	1.35	7.4E-01	AI508146.1	EST_HUMAN	h11409.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
2350	15359	28381	0.93	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3739	16781	29693	18.81	7.4E-01	AF112538.1	NT	Maia puella actin (Act1) mRNA, complete cds
3919	16959	29872	2.01	7.4E-01	AF13310.1	NT	Vibrio cholerae phage CTXphi Calcutta-rsR-a (rsR-a) and Calcutta-rsR-b (rsR-b) genes, complete cds
4340	17367	30250	6.99	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8176	21146	34553	1.04	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8176	21146	34554	1.04	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8980	21946	35370	0.78	7.4E-01	BF346266.1	EST_HUMAN	602018456F1 NCJ_CGAP_Bri67 Homo sapiens cDNA clone IMAGE:4154340 5'
9063	22029		0.64	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9452	22416	35854	7.09	7.4E-01	BE747503.1	EST_HUMAN	601673026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9511	22474	35918	1.14	7.4E-01	AA187986.1	EST_HUMAN	2607001.x1 Stragene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCQP_MOUSE P42692 T-COMPLEX PROTEIN 1, THE TA SUBUNIT ;
10767	23988	37185	0.74	7.4E-01	11424933	NT	SW:TCQP_MOUSE P42692 T-COMPLEX PROTEIN 1, THE TA SUBUNIT ;
12171	25021		4.46	7.4E-01	6753217	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
12284	25101		1.54	7.4E-01	AA72641.1	EST_HUMAN	Mus musculus complement component 1 inhibitor (C1inh), mRNA
3999	17038		0.64	7.3E-01	AP000062.1	NT	h113001.x1 NCJ_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4647	17566	30555	0.97	7.3E-01	AE001168.1	NT	Aeropyrum pernix genome DNA, section 57
							Borrelia burgdorferi (section 52 of 70) of the complete genome

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4726	17749	30841	4.57	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5135	18144	31024	1.18	7.3E-01	Q43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6761	18815	33094	6.03	7.3E-01	L33772.1	NT	Mus musculus antigen (CD72) gene
6761	18815	33095	6.03	7.3E-01	L33772.1	NT	Mus musculus antigen (CD72) gene
7301	23878	33608	0.92	7.3E-01	AJ011418.1	NT	Lysoperoxidase esculentum mRNA for ubiquitin activating enzyme
7692	20650	34014	0.53	7.3E-01	Z14133.1	NT	D melanogaster Cnc mRNA for clathrin heavy chain
7794	20746	34119	7.48	7.3E-01	M28511.1	NT	V alginidylsucrase (scfB) gene, complete cds
7794	20746	34120	7.46	7.3E-01	M28511.1	NT	V alginidylsucrase (scfB) gene, complete cds
8115	21052	34450	0.51	7.3E-01	U34631.1	NT	Mus musculus alpha-4 integrin gene, exon 7
11769	24687	38287	3.11	7.3E-01	AA678019.1	EST_HUMAN	225508.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE431769.3'
11769	24687	38288	3.11	7.3E-01	AA678018.1	EST_HUMAN	225508.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE431769.3'
832	13889		2.03	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1874	14695	27097	3.23	7.2E-01	X79140.1	NT	Nucleosome Nef-4A13 mRNA
2488	15472	28405	1.91	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3080	16137	29048	1.47	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3467	16513	29434	2.44	7.2E-01	AF065006.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-9) gene, vsp417-6(A)-I allele, complete cds
4803	17820	30714	2.69	7.2E-01	D50314.1	NT	L mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
							Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds, and L-type calcium channel alpha)
5159	18168	31048	1.57	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds, and L-type calcium channel alpha)
5159	18168	31047	1.57	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds, and L-type calcium channel alpha)
7421	20388	33739	0.78	7.2E-01	U98033.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8797	21764	35188	1.24	7.2E-01	AF230061.1	NT	Cryptosporidium parvum RING-finger binding protein mRNA, partial cds
9314	22279		0.52	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBNAFD08.5'
10705	23627	37123	2.59	7.2E-01	BF870061.1	EST_HUMAN	602118331 F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE4275331.5'
1091	24051	37574	3.38	7.2E-01	U92623.1	NT	Rattus norvegicus cyclophilin mRNA, complete cds
12523	18343	31291	1.43	7.2E-01	U92568.1	NT	Drosophila melanogaster nematode polyprotein antigen precursor (DVA) mRNA, complete cds
12700	25360		5.56	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 87
683	13755	26895	13.3	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RYR1), complete cds
3075	18132	29045	13.21	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-18

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4236	17266	30151	3.29	7.1E-01	7305360	NT	Mus musculus obogenin (Obog), mRNA
4236	17266	30152	3.29	7.1E-01	7305360	NT	Mus musculus obogenin (Obog), mRNA
6058	19139	32350	1.55	7.1E-01	BF681034.1	EST_HUMAN	602165438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4268344 5'
6058	19139	32351	1.55	7.1E-01	BF681034.1	EST_HUMAN	602165438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4268344 5'
7137	20133	33426	6.92	7.1E-01	U36222.1	NT	Drosophila melanogaster 6-pyruvatecarboxylate synthase (pr) gene, complete cds
8533	21601	34978	0.48	7.1E-01	H64244.1	EST_HUMAN	Y686009.s1 Soares fetal liver spleen TINF3 Homo sapiens cDNA clone IMAGE:202861 3'
9088	22064	35477	0.85	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-30T299-011-409 BT0567 Homo sapiens cDNA
9088	22064	35478	0.85	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-30T299-011-409 BT0567 Homo sapiens cDNA
10214	23139	36628	1.28	7.1E-01	BE904405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10774	23695	37163	1.13	7.1E-01	M12681.1	NT	Human T-cell receptor gamma chain J2 gene
12699	25773	27228	2.34	7.1E-01	AA421492.1	EST_HUMAN	z000h11.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:731109 3'
1233	14270	27228	1.13	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0814 protein, partial cds
1233	14270	27230	1.13	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0814 protein, partial cds
2455	15460	28482	1.09	7.0E-01	N62412.1	EST_HUMAN	Y279e07 s1 Soares, multiple sclerosis, 2N4-HNSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
2455	15460	28483	1.09	7.0E-01	N62412.1	EST_HUMAN	Y279e07 s1 Soares, multiple sclerosis, 2N4-HNSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
5099	18106	37078	2.11	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6062	19143	37944	0.95	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8721	21689	37944	8.51	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9671	22624	38077	0.52	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mUA, mIR, mIF, and mID genes, complete cds
9671	22624	38078	0.52	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mUA, mIR, mIF, and mID genes, complete cds
11454	24397	37943	1.71	7.0E-01	AV768842.1	EST_HUMAN	AV768842 MDS Homo sapiens cDNA clone MDSCHED4 5'
11454	24397	37944	1.71	7.0E-01	AV768842.1	EST_HUMAN	AV768842 MDS Homo sapiens cDNA clone MDSCHED4 5'
13035	25811	31528	1.35	7.0E-01	9630464	NT	Bacteriophage N15 virion, complete genome
971	14023	26976	12.59	6.9E-01	U59674.1	NT	Candida albicans squelene epoxide (CAERG1) gene, complete cds and translational regulator gene, partial cds
971	14023	26977	12.59	6.9E-01	U59674.1	NT	Candida albicans squelene epoxide (CAERG1) gene, complete cds and translational regulator gene, partial cds
1313	14349	27315	2.22	6.9E-01	AA593530.1	EST_HUMAN	rm2a09 at NCL GAP_Gast1 Homo sapiens cDNA clone IMAGE:1085176 3'
3233	16286	29210	1.8	6.9E-01	AE00271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5249	18257	31126	0.92	6.9E-01	AV714502.1	EST_HUMAN	AV714502 DGB Homo sapiens cDNA clone DCBA1D12 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5878	18967	32158	0.8	6.9E-01	AB035692.1	NT	Branchiostoma belcheri BNA3 mRNA for notochord actin, complete cds
6104	19193	32402	0.55	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6506	19570	32822	1.5	6.9E-01	BE280188.1	EST_HUMAN	601177335F1 NIH_MGC_T7 Homo sapiens cDNA clone IMAGE:352328 5'
8312	21281	34592	3.39	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 99
8312	21281	34593	3.39	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 99
9526	22489	37463	0.73	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
10053	22980	38447	0.55	6.9E-01	AF209319.1	NT	Musa acuminata peckate lyase 1 (PL1) mRNA, complete cds
10053	22980	38448	0.55	6.9E-01	AF209319.1	NT	Musa acuminata peckate lyase 1 (PL1) mRNA, complete cds
11587	24525	38061	2.03	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11587	24525	38082	2.03	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
12145	25766		3.91	6.9E-01	Q99569	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFI-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
958	14011	28584	1.52	6.8E-01	AF017784.1	NT	Gardia intestinalis carbamate kinase gene, complete cds
2682	15978		1.26	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome. 2727. 3418852-3573470 aj75605.at Soares, parathyroid, tumor, NB-HPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X56411.1, mri ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
2840	14651	27627	1.5	6.8E-01	AA854475.1	EST_HUMAN	Rat (hooded) prolactin gene, exon iii and flanks
4602	17623	30516	1.75	6.8E-01	J00782.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
6996	22923	36388	1.67	6.8E-01	AB037768.1	NT	Stagonospora avenae bgf1 gene for beta-glucosidase, exons 1-4
11424	24368	37903	1.77	6.8E-01	AJ278675.1	NT	Stagonospora avenae bgf1 gene for beta-glucosidase, exons 1-4
11424	24368	37904	1.77	6.8E-01	AJ278675.1	NT	Stagonospora avenae bgf1 gene for beta-glucosidase, exons 1-4
11450	24393	37938	1.82	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11450	24393	37939	1.82	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11831	24812	38407	1.49	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, lapaen, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds. Sacm21 gene, partial>
11931	24812	38408	1.49	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, lapaen, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds. Sacm21 gene, partial>
298	13392	26320	25.45	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
339	13428	26350	28.03	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1927	14951		1.07	6.7E-01	M12132.1	NT	Quail fast skeletal muscle troponin I gene, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2157	15173	28192	1.79	6.7E-01	AA451864.1	EST_HUMAN	zx12g12.s1 Soares, total, Jctus_N12Hf9_9w Homo sapiens cDNA clone IMAGE:765310 3' similar to contains element TAR1 repetitive element;
2176	15986	28213	2.65	6.7E-01	AF186073.1	NT	Drosophila melanogaster Msl85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
3009	16067	28987	3.96	6.7E-01	6875800	NT	Mus musculus Wiskott-Aldrich syndrome protein (WASP), mRNA
4481	17506	30395	0.78	6.7E-01	X74421.1	NT	S.tuberculosis mRNA for glucose-6-phosphate dehydrogenase
5002	18016	30903	0.97	6.7E-01	AW078110.1	EST_HUMAN	xen59g12.x1 NCI, CGAP, Cor17 Homo sapiens cDNA clone IMAGE:2574598 3'
5587	18693	31651	0.7	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5587	18693	31652	0.7	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6073	19154	32366	0.93	6.7E-01	AE001488.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6456	19521	32771	1.26	6.7E-01	9635035	NT	Galid herpesvirus 2, complete genome
6456	19521	32772	1.26	6.7E-01	9635035	NT	Galid herpesvirus 2, complete genome
7537	20500		4.57	6.7E-01	AE004806.1	NT	Pseudomonas aeruginosa PAO1, section 167 of 528 of the complete genome
7563	20526	33884	0.98	6.7E-01	AE001488.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10503	23425		0.82	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
11300	24250	37776	2.62	6.7E-01	BF354649.1	EST_HUMAN	OM3-HT0769-010600-197-003 HT0769 Homo sapiens cDNA
11787	23942	37464	3.23	6.7E-01	O14357	SWISSPROT	N-ACETYL-GLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI
11989	24847	38444	1.62	6.7E-01	AA342321.1	EST_HUMAN	EST148065 Fetal galeen Homo sapiens cDNA 3' end
2509	18512	28538	1.22	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2711	15705	28721	1.4	6.6E-01	AF196339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3501	19548	29474	1.41	6.6E-01	4506980	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3670	16713	29628	4.37	6.6E-01	Y07693.1	NT	Callicebus random DNA merier, 282bp
4136	17160		0.86	6.6E-01	U9128.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H-L-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5258	18266	31134	1.13	6.6E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
5282	18288	31150	0.95	6.6E-01	Z82002.1	NT	S.pneumoniae pcpB and pcpC genes
5282	18288	31151	0.95	6.6E-01	Z82002.1	NT	S.pneumoniae pcpB and pcpC genes
6466	19531	32779	3.83	6.6E-01	6680577	NT	Mus musculus kinesin light chain 2(Klc2), mRNA
7949	20890	34281	3.57	6.6E-01	AV680508.1	EST_HUMAN	AV680506 GLC Homo sapiens cDNA clone GLCGID04 3'
8912	21878	38304	0.58	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
10023	22960		1.56	6.6E-01	AL103276.2	NT	Homo sapiens chromosome 21 segment HS210078

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12746	25395	31758	1.76	6.6E-01	AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome
624	13689	26906	0.96	6.6E-01	M75140.1	NT	H. vulgatus Na.K-A1Pase alpha subunit mRNA, complete cds
624	13689	26907	0.96	6.6E-01	M75140.1	NT	H. vulgatus Na.K-A1Pase alpha subunit mRNA, complete cds
3446	18493	28412	4.63	6.6E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4311	17340	30220	4.28	6.6E-01	AJ272265.1	NT	Homo sapiens SFP2 gene for secreted phosphoprotein 24 precursor, exons 1-3
5102	18112	30984	3.71	6.6E-01	U29021.1	NT	Phasodius vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5204	18213	31088	1.13	6.6E-01	Z70628.1	NT	H. sapiens mRNA for immunoglobulin heavy chain variable region (3D4-A6, VH4, 4-59/DP-71)
5518	26640	31551	2.13	6.6E-01	P16480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5)
5902	18894	32077	0.58	6.6E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
6887	19639	33234	1.24	6.6E-01	D98343.1	NT	Chicken mRNA for 115-kDa melanocortin matrix protein, complete cds
7841	20768	34163	0.84	6.6E-01	X04769.1	NT	Murine Ig-related lambdaId(30) gene (exon 1) transcribed selectively in pre-B lymphocytes
7920	20873	34262	0.89	6.6E-01	AJ793882.1	EST_HUMAN	W46802.x1 NCL CGAP P228 Homo sapiens cDNA clone IMAGE:2321642.3
10197	23122		1.03	6.6E-01	I75904.1	EST_HUMAN	y421504.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:108847.3
10699	23821	37117	2.2	6.6E-01	AF119876.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10997	23963	37487	2.19	6.6E-01	H87583.1	EST_HUMAN	yu1706.r1 Soares_filicenta_805weeks_2NBP89b9W Homo sapiens cDNA clone IMAGE:262515.5
11045	24009	37635	2.88	6.6E-01	AA601287.1	EST_HUMAN	nc15607.a1 NCL CGAP Phd1 Homo sapiens cDNA clone IMAGE:1100748.3
11143	24103		3.43	6.6E-01	AU138078.1	EST_HUMAN	AL138078 PLAGE1 Homo sapiens cDNA clone PLAGE:1007610.5
11926	24806	38399	2.3	6.6E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
11970	24848	38445	1.47	6.6E-01	AF146687.1	NT	Fugu rubripes U2 small nuclear ribonucleoprotein auxiliary factor subunit-related protein (U2AF1-RS2), 19 kDa Gagi adaptor protein adaptin (AP19), and phosphorylase kinase alpha 2 subunit (PHK42) genes, complete cds; kelch protein (KELCH1) and kelch 2
12130	24999	38604	1.81	6.6E-01	AL161580.2	NT	Anabidopsis thaliana DNA chromosome 4, contig fragment No. 76
12554	25276		2.56	6.6E-01	BE465050.1	EST_HUMAN	h74410.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:3179130.3
252	13349	26275	10.51	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dyshin light chain mRNA, complete cds
3470	16516	26437	3.26	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3875	16974	26623	1.34	6.4E-01	AB043827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4519	17544	30430	0.89	6.4E-01	Y12488.1	NT	M. musculus vrn gene
4519	17544	30431	0.89	6.4E-01	Y12488.1	NT	M. musculus vrn gene
5192	18201	31073	1	6.4E-01	H65337.1	EST_HUMAN	ys90608.r1 Soares retina N2559HR Homo sapiens cDNA clone IMAGE:222096.5
8890	21928	35353	1.57	6.4E-01	AE001247.1	NT	Trepnema pallidum section 63 of 87 of the complete genome

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10449	23371	38863	6.94	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10454	23386	38879	1.18	6.4E-01	BF57040.5.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291128 5'
12656	25342		5.76	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGC008 5'
434	13508	25442	3.27	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
536	13607	25525	2.19	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2171	15187	25208	3.4	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigenic resistance locus
2563	15584	28603	2.72	6.3E-01	U76331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2583	15584	28604	2.72	6.3E-01	U76331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3029	16087		0.8	6.3E-01	Y17275.1	NT	Lycopodium obscurum p8a gene, complete CDS
6182	19257	32490	0.87	6.3E-01	BE043906.1	EST_HUMAN	PMO-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA
6753	19807	33088	1.07	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mg) gene, complete cds
6753	19807	33089	1.07	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mg) gene, complete cds
8856	21833		3.17	6.3E-01	BE902044.1	EST_HUMAN	801676869F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3856351 5'
9238	22304	35636	0.8	6.3E-01	S62927.1	NT	glycoprotein IIIa (AII) 1 and 3 fusion junction [human, Genomic Mutant, 300 nt]
9675	22537	35699	0.74	6.3E-01	BF216984.1	EST_HUMAN	801884080F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102586 5'
9775	22716	38171	2.86	6.3E-01	962762.1	NT	Varicella virus, complete genome
9775	22716	38172	2.86	6.3E-01	962762.1	NT	Varicella virus, complete genome
10298	23223		0.93	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10762	23713	37215	1.55	6.3E-01	Z739003.1	NT	S. cerevisiae chromosome VII reading frame ORF_YGR218w
10895	23815	37322	0.98	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
11400	24345	37878	1.52	6.3E-01	AA87715.1	EST_HUMAN	nr09008.s1 NC1_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 O02916
11863	24599	38173	6.95	6.3E-01	AI004160.1	EST_HUMAN	HLAR.
11754	24882	38281	1.79	6.3E-01	PA47003	SWISSPROT	CM-BT043-080299-046 BT043 Homo sapiens cDNA
11915	24706	38387	2.09	6.3E-01	P38073	SWISSPROT	HYPOTHEICAL 13.7 KD PROTEIN IN INOH-IDS2 INTERGENIC REGION
12258	25225	31308	5.44	6.3E-01	9910293	NT	HYPOTHEICAL 16.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
12359	25149		1.81	6.3E-01	AF105227.1	NT	Mus musculus keratin complex 2, gene 5g (K12-5g), mRNA
12570	25545		3.19	6.3E-01	X83528.1	NT	Homo sapiens 3'-phosphoadenosine 5-phosphatase synthetase (PAPSS) mRNA, complete cds
5970	19055	32255	2.37	6.2E-01	Q10135	SWISSPROT	C. limicola pscD gene
7737	20692		2.75	6.2E-01	AF022253.1	NT	HYPOTHEICAL 142.5 KD PROTEIN C28E2.02 IN CHROMOSOME I
7791	25690	34117	1.12	6.2E-01	AL021127.2	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
8644	21612	35034	5.41	6.2E-01	H72255.1	EST_HUMAN	Mus musculus chromosome X contig; putative Magas9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
							ys0r1e08.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:213542 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9208	22174	35605	0.54	6.2E-01	AF034411.1	NT	Lycopodium esculentum cytosolic Cu Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase dehydratase/dehydratase:NADP oxidoreductase gene, complete cds
9804	21127	34531	1.87	6.2E-01	BE562887.1	EST_HUMAN	601338146F1 NIH_JMGC_44 Homo sapiens cDNA clone IMAGE3690010 5'
9888	22804		2.17	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
10438	23360	38848	7.04	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10602	23822	37332	5.32	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOLE PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
10602	23822	37333	5.32	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOLE PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2404	15411		5.9	8.1E-01	B878078	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc) mRNA
5614	18710	31888	1.3	6.1E-01	M58940.1	NT	Caenorhabditis elegans N2 Cehydo (hlt-1) alternatively spliced genes, complete cds
7053	20075	33382	3.54	6.1E-01	M84733.1	NT	Rat TRPM-2 gene, complete cds
7053	20075	33383	3.54	6.1E-01	M84733.1	NT	Rat TRPM-2 gene, complete cds
7218	20288	33572	0.7	8.1E-01	AW105853.1	EST_HUMAN	xc50103.1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE2587237 3' similar to gb:U12871.1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7312	20283	33624	0.64	8.1E-01	Q63769	SWISSPROT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8575	21543	34983	3.66	6.1E-01	AF033335.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9147	22113	35537	1.17	6.1E-01	11431085	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9147	22113	35538	1.17	6.1E-01	11431085	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9770	22711	36185	23.08	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10202	23127	36613	0.99	6.1E-01	AF236117.1	NT	Pseudomonas aeruginosa PAO1, section 13 of 529 of the complete genome
10408	23328	36812	1.53	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11308	24266		1.91	6.1E-01	X74807.1	NT	P sodium mdh mRNA for chloroplast malate dehydrogenase (NADP+)
12041	24916	38510	1.63	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12041	24916	38511	1.63	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12355	25731	31615	2.77	6.1E-01	A8041350.1	NT	Mus musculus Col4a5 mRNA for type IV collagen alpha 5 chain, complete cds
495	13587	26490	1.41	6.0E-01	D87673.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
563	13583		2.75	6.0E-01	5602869	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLZ2), mRNA
1384	14398	27389	1.92	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH89-593 attachment protein (G) gene, complete cds
3628	18688	28770	0.9	6.0E-01	AJ233366.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4217	17249		1.61	6.0E-01	AF098895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
4279	17308	30187	0.89	6.0E-01	AB028319.1	NT	Yaba monkey tumor virus DNA, BamH1 restriction fragment E, M and partial C, partial and complete cds
5353	18458	31327	2.14	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5514	18614	31547	2.22	6.0E-01	AW139713.1	EST_HUMAN	U1-H-B1-asb-e-10-Q-U1.s1 NC1 CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6889	19746	33022	2.68	6.0E-01	U36813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6818	19872	33161	0.67	6.0E-01	Q04912	SWISSPROT	MAGROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
6988	20211	33539	0.78	6.0E-01	L10234.1	NT	(CDW136) ANTIGEN
6988	20211	33540	0.78	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7577	20539	33698	5.51	6.0E-01	AL277861.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8461	21430	34847	4.95	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8461	21430	34848	4.55	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10182	23107	36589	1.84	6.0E-01	AB006183.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10638	23558		1.56	6.0E-01	Q01487	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PERO (PEROXIN-3)
10748	23671		0.46	6.0E-01	BE837779.1	EST_HUMAN	RC2-FN0094-190700-017-408 FN0094 Homo sapiens cDNA
11878	24760	38346	2.78	6.0E-01	AI420623.1	EST_HUMAN	108107.x1 NC1 CGAP_P228 Homo sapiens cDNA clone IMAGE:2086621 3'
12639	25322	31788	1.97	6.0E-01	11421683	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3) mRNA
12731	25384		2.78	6.0E-01	AA706087.1	EST_HUMAN	236905.s1 Soares, fetal liver, spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:462776 3'
12918	25777	31522	4.71	6.0E-01	905503	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12947	25715		3.4	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
1002	14053	27009	0.97	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 183 of the complete genome
3283	16337	29256	4.95	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3283	16337	29257	4.95	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4260	17279		4.09	5.9E-01	AF162756.1	NT	Rattus norvegicus cecatin 2 mRNA, partial cds
6809	19867	32643	1.45	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7481	20447	33803	2.44	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
8332	21301	34718	0.46	5.9E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 157/6893-1719843
8885	21951	35375	0.48	5.9E-01	D12922.1	NT	Lagonella pneumophila gene for iron superoxide dismutase, complete cds
9901	22853	36314	0.89	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain KUW31/Cx major outer membrane protein (omp1) gene, complete cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10273	23188		0.68	5.9E-01	P06463	SWISSPROT	56 PROTEIN
10548	23470	38666	1.19	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHelial-CADHERIN PRECURSOR (VE-CADHERIN)(CADHERIN-5)
11031	23985	37523	2.46	5.9E-01	Q9X083	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
11037	24001	37528	49.9	5.9E-01	AF167944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11309	24269	37785	2.49	5.9E-01	AF167944.1	EST_HUMAN	PM1-DT0041-190100-002-005 DT0041 Homo sapiens cDNA
11328	24487	38021	1.53	5.9E-01	AF064526.1	NT	Mus speratus strain SPRET/EI CB49 antigen (Ccl48) gene, partial cds
12297	25108	37838	2.43	5.9E-01	L43220.1	NT	Oryzodagium cuniculus alpha 1 anti-trypsin (alpha 1 A1) gene, promoter region
12541	25284		2.86	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for oridine-5'-phosphate decarboxylase, complete cds
12740	25390		6.24	5.9E-01	P34928	SWISSPROT	MITOTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1924	14948	27944	1.28	5.9E-01	P40472	SWISSPROT	SIM1 PROTEIN
2371	15572	28592	1	5.9E-01	7305230	NT	Mus musculus low density lipoprotein B (Ldlb) mRNA
4009	17048	29954	1	5.9E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4078131 5'
4542	17585	30452	4.23	5.9E-01	AB006077.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
5448	18550		0.84	5.9E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5609	18705	31882	0.75	5.9E-01	Q10689	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6308	19379	32818	1.82	5.9E-01	D78659.1	EST_HUMAN	HUI5005088 Human placenta polyA+ (TF-1) Homo sapiens cDNA clone GEN-500508 5'
6445	19510	32780	0.73	5.9E-01	D50601.1	NT	Shigella sonnei Human DNA for 28 ORF 5, complete cds
6985	20208		2.55	5.9E-01	S65091.1	NT	Cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8219	21188		2.63	5.9E-01	H41571.1	EST_HUMAN	yr91403.s1 Scores adult brain N2b5HB5Y Homo sapiens cDNA clone IMAGE:175757 3' similar to
8423	21382	34802	0.59	5.9E-01	A1280051.1	EST_HUMAN	gb-S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8423	21392	34803	0.59	5.9E-01	A1280051.1	EST_HUMAN	gb-S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8532	21500	34916	2.97	5.9E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8532	21500	34917	2.57	5.9E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
9243	22209	35640	9.77	5.9E-01	A1270774.1	NT	Homo sapiens partial TGF-4 gene for T-cell transcription factor-4, exons 6-11
9323	22288	35718	1.02	5.9E-01	Q27068	SWISSPROT	TRANSCRIPTION FACTOR E2F
9324	22288	35719	0.48	5.9E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE 1F48F22 IN CHROMOSOME X
9954	22881		0.81	5.9E-01	BF031606.1	EST_HUMAN	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827288 5'
11334	24324	37808	6.9	5.9E-01	AJ43213.1	NT	Homo sapiens partial 5-HT14 receptor gene, exons 2 to 5
11373	24320		2.89	5.9E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'
11478	24419		1.81	5.9E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'
1482	14325	27498	1.11	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN AIV PRECURSOR (APO-AIV)
1492	14525	27497	1.11	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN AIV PRECURSOR (APO-AIV)
3056	18113		0.77	5.7E-01	6755233	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1) mRNA

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3237	16292	28214	1.38	5.7E-01	Q8WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVOT1) (MOVOT1)
3515	16861		2.79	5.7E-01	AB033503.1	NT	Populus euphratica pease-2 mRNA for 1-aminocyclopentane-1-carboxylate synthase, complete cds
3922	16862	29875	1.05	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV6S7-2-BT5T) mRNA, partial cds
5213	18222	31087	11.22	5.7E-01	4595050	NT	Homo sapiens lymphocyte antigen 8 complex, locus H (LY8H) mRNA
6490	18565	32805	4.36	5.7E-01	BF035413.1	EST_HUMAN	601454982F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3858590 5'
6869	19022	33218	0.82	5.7E-01	AA194201.1	EST_HUMAN	z338406.t1 Source: NIH/MPu.S1 Homo sapiens cDNA clone IMAGE:665674.5'
7042	18374	31282	1.3	5.7E-01	AL111440.1	NT	Bcl-2b chinea strain T4 cDNA library under conditions of nitrogen deprivation
8041	20578	34374	2.13	5.7E-01	P00873	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
8303	21272		0.51	5.7E-01	AJ251835.1	NT	Mus musculus Kcnq1, L-type, Mch2, Tesc-1, Tesc4 and Tesc8 genes, alternative transcripts
8723	21801		0.52	5.7E-01	AJ065051.1	EST_HUMAN	HIA0895 Human fetal liver cDNA library Homo sapiens cDNA
10159	23084	36550	1.22	5.7E-01	AL161522.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10159	23084	36561	1.22	5.7E-01	AL161522.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10940	23960	37376	0.75	5.7E-01	BF540962.1	EST_HUMAN	502067712F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4066610 5'
12252	25078		1.49	5.7E-01	BE715051.1	EST_HUMAN	MR3-1T0736-180700-003-a02 H10736 Homo sapiens cDNA
1859	14914	27907	1.6	5.6E-01	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
1859	14914	27908	1.6	5.6E-01	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
3378	16426	26351	1.53	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3378	16426	26352	1.53	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4298	17267	30174	0.77	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
5205	18214	31089	0.93	5.6E-01	BF032377.1	EST_HUMAN	601452855F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3856717 5'
9155	22121	35550	14.86	5.6E-01	AV584703.1	EST_HUMAN	AV584703 GK HG Homo sapiens cDNA clone GKGFSP05 5'
9155	22121	35551	14.86	5.6E-01	AV584703.1	EST_HUMAN	AV584703 GK HG Homo sapiens cDNA clone GKGFSP05 5'
9730	22759	36211	1.23	5.6E-01	AB039782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
12153	25011		3.4	5.6E-01	BE386280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
12270	25092	38176	1.73	5.6E-01	AA498535.1	EST_HUMAN	np75g10.s1 NCI CGAP_P48 Homo sapiens cDNA clone IMAGE:940674 similar to contains element P1R7 repetitive element
12638	18341	31290	1.51	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12662	25340		3.06	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
13060	25536		4.95	5.6E-01	BF573829.1	EST_HUMAN	602130202F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
13110	25630		1.33	5.6E-01	AA663881.1	EST_HUMAN	ae74b04.g1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:969871 3'
1216	14254	27212	0.82	5.6E-01	8893912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pcbb) mRNA
2712	16706	28722	5.31	5.6E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2712	15706	28723	5.31	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2829	15987	28908	0.78	5.5E-01	5902085	NT	Homo sapiens superkiller viral-like protein 2 (S. cerevisiae homolog)-like (SKIVL), mRNA
3079	16139		1.48	5.5E-01	H46219.1	EST_HUMAN	yo19a10.1.1 Sources adult brain N2b-H185V Homo sapiens cDNA clone IMAGE:178268 3'
3243	16303	26227	4.75	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3704	16747	25661	2.24	5.5E-01	P48756	SWISSPROT	FOS-RELATED ANTIGEN-1
5209	18218	31094	1.06	5.5E-01	U90097.1	NT	Bos taurus MHC class II beta-chain BoLA-DIB1 gene, partial cds
7467	20433	33789	0.58	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region/butyrophilin-like protein gene, partial cds; Nidm4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete cds
7467	20433	33790	0.58	5.5E-01	AF030001.1	NT	Nidm4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete cds
7504	20469		0.67	5.5E-01	AB015596.1	NT	Carassius auratus gape for gonadotropin II beta subunit, complete cds
~ 8792	21759	35181	0.66	5.5E-01	A1791766.1	EST_HUMAN	alpha2001 y6 NCL CGAP Lu5 Homo sapiens cDNA clone IMAGE:1602338 5'
10725	23051		0.69	5.5E-01	U88415.1	NT	Chinese-Congo hemorrhagic fever virus strain SPU 415/85 nucleocapsid protein gene, complete cds
10743	23685	37160	0.87	5.5E-01	T05047.1	EST_HUMAN	EST1028335 Fetal brain, Stratagene (carr938206) Homo sapiens cDNA clone HFBCQ35
146	13249	26178	9.02	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
146	13249	26179	9.02	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
587	13655	26599	1.34	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GSA (gsa) genes, complete cds; and unknown genes
587	13655	26599	1.34	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GSA (gsa) genes, complete cds; and unknown genes
587	13655	26570	1.34	5.4E-01	AF232006.1	NT	QVY-NN0040-070400-160-304 NN0040 Homo sapiens cDNA
1276	14311	27272	2.99	5.4E-01	AW890087.1	EST_HUMAN	Chlamydia pneumoniae AFR39, section 74 of 84 of the complete genome
2116	15133		2.81	5.4E-01	AE002247.2	NT	Drosophila melanogaster mRNA for 15.15 beta carotene dioxygenase (beta-dio gene)
2265	15279	28304	2.26	5.4E-01	AJ276982.1	NT	PM22-CN030-030200-003-c10 CN0300 Homo sapiens cDNA
5740	18834	32014	0.91	5.4E-01	AW842327.1	EST_HUMAN	Rattus norvegicus gene for TIS11, complete cds
6315	18386	32628	0.8	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
7226	20248	33582	0.77	5.4E-01	BE968692.2	EST_HUMAN	60166027671 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3'
7558	20521	33877	0.76	5.4E-01	Z21619.1	NT	S. cerevisiae RUB3 gene encoding DBP synthase
7558	20521	33878	0.76	5.4E-01	Z21619.1	NT	S. cerevisiae RUB3 gene encoding DBP synthase

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7590	20523	33881	1.78	5.4E-01	Q6428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) (INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE)
10349	23273		1.93	5.4E-01	BF572338.1	EST_HUMAN	
11414	24358	37893	2.19	5.4E-01	P36958	SWISSPROT	INTRATE REDUCTASE [NADPH] (NR)
11652	24889	38150	1.82	5.4E-01	AW376894.1	EST_HUMAN	QVA-BT0036-271299-089-h04 B0536 Homo sapiens cDNA
11941	24821	39416	3.29	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11941	24821	39417	3.29	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
12215	25054		3.88	5.4E-01	A189398.1	EST_HUMAN	w37g04.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:U13452 LAMIN A (HUMAN);
517	13588	26508	1.86	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21- hydroxylase (CYP21B), complement component C4 (C4B), G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes >
2150	15166	28182	0.97	5.3E-01	AF13918.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2150	15166	28183	0.97	5.3E-01	AF13918.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2764	15786	28803	8.62	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2764	15786	28804	8.62	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3257	16311	29222	3.25	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds
4239	17268		1.33	5.3E-01	U39887.1	NT	Myoplasma genitalium section 9 of 51 of the complete genome
5533	18631	31569	2.06	5.3E-01	A1820621.1	EST_HUMAN	zu42h12.y6 Soares ovary tumor NB-HOT Homo sapiens cDNA clone IMAGE:740711 5'
5533	18631	31570	2.06	5.3E-01	A1820621.1	EST_HUMAN	zu42h12.y6 Soares ovary tumor NB-HOT Homo sapiens cDNA clone IMAGE:740711 5'
5633	18729	31880	0.76	5.3E-01	AA180672.1	EST_HUMAN	zr42g09.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5633	18729	31881	0.76	5.3E-01	AA180672.1	EST_HUMAN	zr42g09.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5729	18823	32003	2	5.3E-01	BEG45620.1	EST_HUMAN	7a73c12.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5729	18823	32004	2	5.3E-01	BEG45620.1	EST_HUMAN	7a73c12.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9255	22221		1.84	5.3E-01	L01950.2	NT	Roridia gorgonias ribulose 1,5-bisphosphate carboxylase (bcl), gene, partial cds; chloroplast gene for chloroplast product
9307	22272	35703	0.76	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element;
9307	22272	35704	0.76	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element;

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10572	23494	36986	0.74	5.3E-01	AI054210.1	EST_HUMAN	w34b02.xt NCI CGAP_Maf15 Homo sapiens cDNA clone IMAGE:2851275 3' similar to SW:COXA_HUMAN P20874 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
10877	23897	37410	0.19	5.3E-01	11428833	NT	Homo sapiens nucleophosin 21 NUP214 (CAN) (NUP214), mRNA
11886	24787	38354	5.17	5.3E-01	BE566291.1	EST_HUMAN	601338067.F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 3'
12144	25775		4.97	5.3E-01	AA916053.1	EST_HUMAN	og30605.st NCI CGAP_B77 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gpJ02611 APOLOPROTEIN D PRECURSOR (HUMAN);
817	13875	26823	16.24	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1188	14209	27163	7.88	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-A15) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1195	14235	27190	3.01	5.2E-01	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
1903	14927		3.19	5.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2156	15172	26191	2.36	5.2E-01	AB018263.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3136	16163	29102	1.57	5.2E-01	U65942.1	NT	Chlamydomonas reinhardtii strain S2838 POLIP21A and POMPOA precursor, genes, complete cds
3251	16306		1.14	5.2E-01	D73443.1	NT	Azotobacter vinelandii tad gene for isocitrate dehydrogenase, complete cds
3416	16464		1.39	5.2E-01	AL116780.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3458	16504	29424	2.72	5.2E-01	AA984165.1	EST_HUMAN	em71605.st Stratiagene schizos brain S11 Homo sapiens cDNA clone IMAGE:1615504 3'
3648	16681		1	5.2E-01	AF020259.1	NT	Medicago sativa chloroplast maleate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
5180	18169		1.04	5.2E-01	AF020259.1	NT	Homo sapiens chromosome 21 segment HS21C081
5739	18830	32008	1.02	5.2E-01	AA284261.1	EST_HUMAN	zc44d06.T7 Soares_senescent_fibroblasts NHRSF Homo sapiens cDNA clone IMAGE:325169 3'
10088	25700	39489	0.84	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10088	25700	39490	0.84	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10282	29217	36731	0.52	5.2E-01	AA194518.1	EST_HUMAN	z05b08.r1 Stratiagene muscle 637/209 Homo sapiens cDNA clone IMAGE:628793 5'
10387	23309	36787	1.76	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
13031	29578		6.62	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
819	13694	26502	2.34	5.1E-01	M58509.1	NT	Human actinoprotein reductase gene, exons 3 to 12
849	13715	26526	3.53	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pt vt1) 16S rRNA gene
849	13715	26537	3.53	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pt vt1) 16S rRNA gene
1660	14692		1.28	5.1E-01	X67885.1	NT	R.nervigicus mRNA for mammalian fusca protein
4103	17137	30032	4.81	5.1E-01	AI858495.1	EST_HUMAN	w139572.xt NCI CGAP_UH Homo sapiens cDNA clone IMAGE:2427263 3'
4216	17245	30130	2.99	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
8248	19417	32658	0.87	5.1E-01	BE541068.1	EST_HUMAN	601063806.F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6407	19478		0.83	5.1E-01	AV172236.1	EST_HUMAN	AV172236 DCA Homo sapiens cDNA clone DCAAU07 5'

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7102	20036	33339	1.52	5.1E-01	R00873.1	EST_HUMAN	y84a09.s1 Scores Placenta Nb2-IP Homo sapiens cDNA clone IMAGE:146872 3'
8818	21884	33309	0.62	5.1E-01	AW608881.1	EST_HUMAN	QVA-S10023-160400-172-401 S10023 Homo sapiens cDNA
8818	21884	33310	0.62	5.1E-01	AW608881.1	EST_HUMAN	QVA-S10023-160400-172-401 S10023 Homo sapiens cDNA
10043	22970	36437	4.3	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
10046	22973	36440	3.2	5.1E-01	IW22302.1	EST_HUMAN	68B1 Human retina cDNA 12509-cleaved sublibrary Homo sapiens cDNA not directional
10521	23443	36941	0.89	5.1E-01	M94578.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12284	25088	38174	2.09	5.1E-01	BF540777.1	EST_HUMAN	602067471F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068744 5'
12368	25709		2.47	5.1E-01	BF030207.1	EST_HUMAN	60155883F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'
12811	26310		3.62	5.1E-01	BF439882.1	EST_HUMAN	huc5110.XT NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element
2144	15161	28176	0.97	5.0E-01	4895552	NT	TAK1 repetitive element
2144	15161	28177	0.97	5.0E-01	4895552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2154	15170	28187	2.39	5.0E-01	AF008210.1	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2154	15170	28188	2.39	5.0E-01	AF008210.1	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2172	15188		0.91	5.0E-01	AL161832.2	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEF), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene
3751	18802	29714	0.8	5.0E-01	U95574.1	NT	Arabisopsis thaliana DNA chromosome 4, contig fragment No. 33
3842	18882	29786	1	5.0E-01	L38483.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3887	18927	29835	2.74	5.0E-01	AB033010.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
6801	18855		0.64	5.0E-01	BF576188.1	EST_HUMAN	Homo sapiens mRNA for KIAA1184 protein, partial cds
7026	20869	34256	0.68	5.0E-01	AL161549.2	NT	602132642F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271839 5'
7926	20869	34257	0.66	5.0E-01	AL161549.2	NT	Arabisopsis thaliana DNA chromosome 4, contig fragment No. 49
8875	21842		1.87	5.0E-01	M92304.1	NT	Arabisopsis thaliana DNA chromosome 4, contig fragment No. 49
9018	21984	35404	0.59	5.0E-01	BF107848.1	EST_HUMAN	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
9813	21136	34538	3.18	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
9883	22910	36375	1.31	5.0E-01	P35573	SWISSPROT	GLYCOSYL DEBRANCHING ENZYME (GLYCOSYL DEBRANCHER) (INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCAN TRANSFERASE); AMYLLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE))
9883	22910	36376	1.31	5.0E-01	P35573	SWISSPROT	GLYCOSYL DEBRANCHING ENZYME (GLYCOSYL DEBRANCHER) (INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCAN TRANSFERASE); AMYLLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE))

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10756	23676		1.38	5.0E-01	BE689218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849438 5'
12302	25113		6.28	5.0E-01	AF028215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
13004	25558		2.21	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
13011	25553		5.9	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
790	13849	26798	2.03	4.9E-01	BE571462.1	EST_HUMAN	602076949F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1088	14700	27676	2.37	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1821	14946	27941	0.99	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-A) mRNA, complete cds
5480	19590	31491	1.43	4.9E-01	Q61854	SWISSPROT	FIBRILLIN 1 PRECURSOR
6153	19228	32457	2.67	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6153	19228	32458	2.67	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7685	20643	34007	1.69	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7972	20911	34301	0.7	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYL TRANSFERASE
7972	20911	34302	0.7	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYL TRANSFERASE
9341	22306		1.77	4.9E-01	BF209781.1	EST_HUMAN	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
9542	22505	35954	0.99	4.9E-01	AW339905.1	EST_HUMAN	hs06c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907286 3' similar to TR.O95714
9651	25008		2.64	4.9E-01	10946883	NT	065714 HERC2 ;
10681	23603	37097	0.86	4.9E-01	AF063960.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13n1), mRNA
10888	23808	37314	0.57	4.9E-01	X90000.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
12196	25041		1.41	4.9E-01	AF178912.1	NT	H. sapiens DNA for BCL7A gene and BCL7AIGH locus fusion
12897	25953		6.43	4.9E-01	AA613562.1	EST_HUMAN	Homo sapiens neurotrophin-1(B)-cell stimulating factor-3 gene, complete cds
5585	18681	31649	8.83	4.8E-01	J02987.1	NT	nc22a11.s1 NCI CGAP Cc10 Homo sapiens cDNA clone IMAGE:1144652 3'
8839	19839	33184	0.69	4.8E-01	U92882.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
8846	19899		3.82	4.8E-01	AA659878.1	EST_HUMAN	Mus musculus slow skeletal muscle troponin T (Tnni1) gene, complete cds
7538	20501		1.98	4.8E-01	5031660	NT	Homo sapiens reproduction 8 (OR52285E) mRNA
7829	20872	34281	0.78	4.8E-01	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8037	20974	34369	3.56	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8037	20974	34370	3.56	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8237	21208	34611	0.98	4.8E-01	AB20744.1	EST_HUMAN	W7710.95 Soares breast 2N4b1Bst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element
6900	22604		0.67	4.8E-01	BE155748.1	EST_HUMAN	PM1-HT0360-201299-004-004-HT0360 Homo sapiens cDNA
10398	23291		0.56	4.8E-01	BF596933.1	EST_HUMAN	602184267F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
11081	24043		1.75	4.8E-01	X83502.1	NT	S. cerevisiae ORFs from chromosome X



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12277	25096		1.65	4.8E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12503	25371		3.32	4.8E-01	AF227565.1	NT	1 pparalpha crizl transposon VIP II SIRE repeat region
13088	25766		1.49	4.8E-01	AJ152984.1	NT	Chlamydomonas reinhardtii cop gene, exons 1-5
6864	19721	32896	8.88	4.7E-01	BF217173.1	EST_HUMAN	601863880F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:4098387 5'
7241	19876	33273	0.92	4.7E-01	AJ204374.1	EST_HUMAN	qf72a09.x1 Soares_testic_NHT Homo sapiens cDNA clone IMAGE:175544 3'
8197	21167	34577	0.59	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8197	21167	34578	0.59	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
6430	22394	35834	0.57	4.7E-01	69815071	NT	Rattus norvegicus Spermathe binding protein (Sbp), mRNA
11193	24148		4.76	4.7E-01	AF102873.1	NT	Influenza A virus isolate h661687 hemagglutinin (HA) gene, partial cds
11422	24366	37901	1.78	4.7E-01	U11069.1	NT	Human collagen alpha2(X)(COL11A2) gene, exons 6 through 16, and partial cds
11613	24551	38111	1.74	4.7E-01	BF529658.1	EST_HUMAN	602043889F1 NCI CGAP Brn67 Homo sapiens cDNA clone IMAGE:4181303 5'
11704	24669	38246	1.49	4.7E-01	AW889448.1	EST_HUMAN	RCB-NT0029-240400.011.E08 NT10029 Homo sapiens cDNA
12999	25173		1.53	4.7E-01	BE887763.1	EST_HUMAN	601611333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
3756	18798	29709	1.53	4.6E-01	BF693300.1	EST_HUMAN	602163926F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4264874 5'
3756	18798	29710	1.53	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5190	18196		0.93	4.9E-01	M11267.1	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
5463	18593	31503	1	4.6E-01	BF131593.1	EST_HUMAN	601600234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5463	18593	31504	1	4.6E-01	BF131593.1	EST_HUMAN	601600234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5548	18645	31586	3.33	4.9E-01	Q90643	SW/ISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5548	18645	31587	3.33	4.9E-01	Q90643	SW/ISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5925	18721	31860	1.95	4.9E-01	BE734781.1	EST_HUMAN	601569755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5639	18735	31867	3.12	4.9E-01	AJ247979.1	EST_HUMAN	qf56h02.x1 Soares_fetal_liver_spleen_TNF.LS_51 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5639	18735	31868	3.12	4.9E-01	AJ247979.1	EST_HUMAN	qf56h02.x1 Soares_fetal_liver_spleen_TNF.LS_51 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5647	18743	31909	1.46	4.9E-01	P20050	SW/ISSPROT	TR-O15338 O15338 BUTYROPHILIN ;
5730	18824		0.95	4.9E-01	AF212124.1	NT	MEIOSIS SPECIFIC PROTEIN HOP1
5821	18811		0.78	4.9E-01	BE81247.1	EST_HUMAN	Andis schwarzi cyclochrome b gene, partial cds; mitochondrial gene for mitochondrial product
6002	19085	32285	0.51	4.9E-01	D26215.1	NT	PMB-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6388	19454	32699	0.92	4.9E-01	AE000894.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6881	19933	33231	0.52	4.9E-01	AF115340.1	NT	Methanobacterium thermoautotrophicum from bases 1165761 to 1176238 (section 100 of 148) of the complete genome
							Bacillus subtilis Bbma (bbma) gene, complete cds

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6832	20196	33474	1.43	4.8E-01	U62332.1	NT	Emricella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6832	20196	33475	1.43	4.8E-01	U62332.1	NT	Emricella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7441	25681	33759	0.53	4.8E-01	L07320.1	NT	Murine cytomegalovirus s1 protein gene, complete cds
8001	20940	34333	0.78	4.6E-01	AA493877.1	EST_HUMAN	m04H05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element/contains element L1 repetitive element;
8093	21029		0.53	4.6E-01	AE004031.1	NT	Xyella fastidiosa, section 177 of 229 of the complete genome
8893	21831	35052	13.28	4.6E-01	BF667369.1	EST_HUMAN	602130953.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
9099	22065	35400	0.47	4.6E-01	AA892237.1	EST_HUMAN	007808.s1 NCI_CGAP_K45 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9099	22065	35491	0.47	4.6E-01	AA892237.1	EST_HUMAN	007808.s1 NCI_CGAP_K45 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9556	22599	36048	0.99	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9556	22599	36048	0.99	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
10024	22951	36418	0.89	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
10024	22951	36419	0.89	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
10335	23256	36736	1.82	4.6E-01	AB15534.1	EST_HUMAN	wg/3a12.x1 Soares_NSFC_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
10335	23256	36737	1.82	4.6E-01	AB15534.1	EST_HUMAN	wg/3a12.x1 Soares_NSFC_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
11335	24285		2.28	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELL OGENIN RECEPTOR PRECURSOR (YL)
11343	24283	37818	4.94	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11343	24283	37819	4.94	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11445	24388	37930	3.88	4.6E-01	BE272225.1	EST_HUMAN	60112608.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2689663 5'
11769	23954	37476	4.41	4.6E-01	AF018569.1	NT	Human thioridine methyltransferase (TPMT) gene, exon 10 and complete cds
11769	23954	37477	4.41	4.6E-01	AF018569.1	NT	Human thioridine methyltransferase (TPMT) gene, exon 10 and complete cds
12448	25208		1.69	4.6E-01	D53316.1	EST_HUMAN	HUM105F03B Clontech human fetal brain poly(A <sup>+</sup> mRNA (#6633) Homo sapiens cDNA clone GEN-105F03 5'
1718	14748		0.92	4.5E-01	BE511420.1	EST_HUMAN	601142105.F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505963 5'
1825	14950	27946	1.34	4.5E-01	AE001831.1	NT	Deinococcus radiodurans R1 section 88 of 229 of the complete chromosome 1
1825	14950	27947	1.34	4.5E-01	AE001831.1	NT	Deinococcus radiodurans R1 section 88 of 229 of the complete chromosome 1

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2881	15940	28857	5.38	4.9E-01	AA677088.1	EST_HUMAN	2555d02.s1 Sources: fetal_liver, spleen, 1NF1S_51 Homo sapiens cDNA clone IMAGE:454179 3'
3328	16379	29300	3.85	4.9E-01	Q05763	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3389	16438	28364	1.82	4.9E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4080	17006		1.28	4.9E-01	Q25247	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN
4101	17135	30030	1.22	4.9E-01	AI1708908.1	EST_HUMAN	aa89609.x1 Barleed aorta HPLR86 Homo sapiens cDNA clone IMAGE:2353480 3'
4205	18325		4.08	4.9E-01	AW873496.1	EST_HUMAN	h689602.x1 Sources: NFL_1_Q8C_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
4980	17595	30884	1.09	4.9E-01	BE963445.2	EST_HUMAN	60165725R1 NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3866023 3'
5628	18724	31885	1.3	4.9E-01	AW608814.1	EST_HUMAN	OV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
6760	18914		1.74	4.9E-01	Q00958	SWISSPROT	COAT PROTEIN
7644	20504	33669	0.93	4.9E-01	M37036.1	NT	Rat nucleolar proteins B23.1 and B23.2
7867	20811	34188	2.64	4.9E-01	AI858949.1	EST_HUMAN	w32e02.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
7891	20630	34325	0.61	4.9E-01	P50070	SWISSPROT	SWISNF COMPLEX 170 KDA SUBUNIT ;
8650	21013		0.57	4.9E-01	M32651.1	NT	DNA PRIMASE
8746	21714	35137	3.88	4.9E-01	AI848598.1	EST_HUMAN	D melanogaster Shaw2 protein mRNA, complete cds
							1255g11.x1 NCI CGAP_OV65 Homo sapiens cDNA clone IMAGE:2292644 3'
8905	21871	35287	0.74	4.9E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
9133	22099		1.72	4.9E-01	11444788	NT	Homo sapiens hypothetical protein DKFZp947G183 (DKFZp947G183), mRNA
9351	22316	35742	0.78	4.9E-01	AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10300	23225		0.80	4.9E-01	9630816	NT	Bombay mori nuclear polyhedrosis virus, complete genome
10861	23781	37281	26.2	4.9E-01	M80006.1	EST_HUMAN	EST029531 Fetal brain; Striatum (cau#36206) Homo sapiens cDNA clone HFBCY17
10861	23781	37282	26.2	4.9E-01	M80006.1	EST_HUMAN	EST029531 Fetal brain; Striatum (cau#36206) Homo sapiens cDNA clone HFBCY17
11212	24165	37695	2.3	4.9E-01	AW591271.1	EST_HUMAN	xt04h01.x1 NCI CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
12165	25955		5.3	4.9E-01	BE871451.1	EST_HUMAN	Q64282 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
12349	25144		1.48	4.9E-01	Q18638	SWISSPROT	601449201F1 NIH_MGC 95 Homo sapiens cDNA clone IMAGE:3852861 5'
12452	25211		1.54	4.9E-01	AI132045.1	NT	OUT AT FIRST PROTEIN
12891	29478		8.22	4.9E-01	11422098	NT	Thalera annulata sM12 gene
2052	15071		2.23	4.9E-01	6880503	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
							Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA
2398	15405	28430	7.02	4.9E-01	P48765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3328	16377	29288	1.36	4.4E-01	AF098790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3329	16377	29296	1.36	4.4E-01	AF098790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
4262	16381	29302	1.9	4.4E-01	BF056726.1	EST_HUMAN	791-002.Y1 NCL CGAP_Bn16 Homo sapiens cDNA clone IMAGE:3383795 5'
4263	17291		1.75	4.4E-01	BE378707.1	EST_HUMAN	601237139F.1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609383 5'
5634	18594	31505	1.63	4.4E-01	P04829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5494	18594	31506	1.63	4.4E-01	P04829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
6472	18894	32048	1.77	4.4E-01	S65019.1	NT	inulin (beta, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA, partial, 390 nt)
5760	18892	32064	1.82	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLEC Homo sapiens cDNA clone GLECCS12 5'
6064	19145	32356	1.42	4.4E-01	AI198413.1	EST_HUMAN	q182H1.1 NCL CGAP_Bn28 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29169 UNKNOWN PROTEIN ;
6084	19145	32357	1.42	4.4E-01	AI188413.1	EST_HUMAN	q182H1.1 NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29169 UNKNOWN PROTEIN ;
6368	19436	32690	1.9	4.4E-01	AW080795.1	EST_HUMAN	xc27e08.x1 NCL CGAP_Cd48 Homo sapiens cDNA clone IMAGE:2385510 3' similar to TR:Q65154 Q65154 AFLATOXIN B1-ALDEHYDE REDUCTASE ;
6462	19527		1.17	4.4E-01	AA776132.1	EST_HUMAN	aa85d11.at Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M16038 TYROSINE-PROTEIN KINASE LYN (HUMAN);
7077	20587	33950	0.95	4.4E-01	AE000571.1	NT	Helicobacter pylori 26695 section 49 of 134 of the complete genome
8173	21143		12.98	4.4E-01	Z11679.1	NT	S.tuberculosis mRNA for induced stolon tip protein (partial)
9115	22081	35509	0.74	4.4E-01	AA056427.1	EST_HUMAN	Z189a03.x1 Stratagene cdon (893720) Homo sapiens cDNA clone IMAGE:509835 3'
9506	22469	35913	0.72	4.4E-01	AF112540.1	NT	HIV-1 isolate 08107v8 from USA, envelope glycoprotein (env) gene, partial cds
9538	22501	35949	0.56	4.4E-01	AW612578.1	EST_HUMAN	h035c08.x1 NCL CGAP_Kd41 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW:MSH6 HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
9645	22589	36038	1.21	4.4E-01	O62939	SWISSPROT	ZINC FINGER X-CROMOSOMAL PROTEIN
10321	23245	38725	2.1	4.4E-01	AI286850.1	EST_HUMAN	q3809g.x1 NCL CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1910821 3'
10322	23246		3.91	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10457	23379	38872	5.07	4.4E-01	P33590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10740	23562	37156	1.27	4.4E-01	S78404.1	NT	beta-HKA-H-K-ATase beta-subunit (beta, Genomic, 8883 nt, segment 2 of 2)
10740	23562	37157	1.27	4.4E-01	S78404.1	NT	beta-HKA-H-K-ATase beta-subunit (beta, Genomic, 8883 nt, segment 2 of 2)
12432	25168	31824	5.76	4.4E-01	G677874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12651	25435	31727	2.93	4.4E-01	P64725	SWISSPROT	Autographa californica nucleopolydnavirus, complete genome
12967	25635		1.45	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
4111	13484	28419	2.49	4.3E-01	AF155218.1	NT	Callithrix jacchus MWLW opsin gene, upstream flanking region
4111	13484	28420	2.49	4.3E-01	AF155218.1	NT	Callithrix jacchus MWLW opsin gene, upstream flanking region
1607	14639	27616	0.96	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2983	16942		1.83	4.3E-01	AW 835289.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3073	16130	29042	0.94	4.3E-01	AW 998477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4178	17209	30095	1.32	4.3E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4493	13484	28418	1.83	4.3E-01	AF15218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4435	13484	28420	1.83	4.3E-01	AF15218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5154	18184		1.17	4.3E-01	9635250	NT	Xestia c-higum granulovirus, complete genome
5201	18296	31157	1.16	4.3E-01	BE780162.1	EST_HUMAN	60146030F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3871255 5'
5438	18540	31449	0.89	4.3E-01	P48934	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5438	18540	31450	0.89	4.3E-01	P48934	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5960	18075	32273	1.5	4.3E-01	BE181635.1	EST_HUMAN	QV7-HT0638-070500-181-d08 HT0638 Homo sapiens cDNA
6010	19093	32293	1.83	4.3E-01	AF179825.1	NT	Saltilit soluteus olfactory receptor (SSC186) gene, partial cds
6885	18919	33214	4	4.3E-01	AJ001678.1	NT	Caturnix collumix japonica tncg gene
7049	20071		0.88	4.3E-01	Q33367	SWISSPROT	DNA GYRASE SUBUNIT B
7662	20622		1.83	4.3E-01	BF346001.1	EST_HUMAN	602023134F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158296 5'
8116	21053		0.62	4.3E-01	M59843.1	NT	Human lipoprotein associated coagulation inhibitor (LACI) gene, exon 2
8770	21737		2.56	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C1 (flaC-fla) genes, complete cds
9610	22614	36066	1.04	4.3E-01	Y14604.1	NT	Erwinia amylovora resV gene
10064	23011	36483	1.88	4.3E-01	AW 630048.1	EST_HUMAN	ht74e10.y1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2968954 5'
10064	23011	36484	1.88	4.3E-01	AW 630048.1	EST_HUMAN	ht74e10.y1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2968954 5'
10589	23511	37005	0.85	4.3E-01	AW 170559.1	EST_HUMAN	xh3e35x1 Soares_NHCC, cervical, tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
10878	23769	37301	0.48	4.3E-01	AF65292.1	EST_HUMAN	TR000168 000189 MU-ADAPTIN-RELATED PROTEIN 2. ;
11277	20178	33603	1.85	4.3E-01	AF075628.1	NT	yr4506.5 s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2082509 3'
11539	24480	38031	1.77	4.3E-01	AW 693658.1	EST_HUMAN	RC3-BN0034-280200-013-c12 BN0034 Homo sapiens cDNA
11539	24480	38032	1.77	4.3E-01	AW 693658.1	EST_HUMAN	RC3-BN0034-280200-013-c12 BN0034 Homo sapiens cDNA
13055	25592		2.24	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor wnh gene
1360	15665	27365	1.77	4.2E-01	Q38102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3623	16666	29380	4.43	4.2E-01	AE003847.1	EST_HUMAN	Xyella fastidiosa, section 93 of 229 of the complete genome
3651	16824	29609	1.04	4.2E-01	AJ280338.1	EST_HUMAN	q9a401.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879445 3'
3724	18324		1.22	4.2E-01	N81203.1	EST_HUMAN	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E-1-K similar to R07879, Z0408
3883	16933	28943	0.89	4.2E-01	AW 835527.1	EST_HUMAN	QV0-LT0015-180200-127-H01 LT0015 Homo sapiens cDNA
4007	17046	28953	1.72	4.2E-01	Q04886	SWISSPROT	SOX9 PROTEIN
4726	17746	30637	4.9	4.2E-01	AA534093.1	EST_HUMAN	h9h9i01.s1 NCI_CGAP_P710 Homo sapiens cDNA clone IMAGE:997777 similar to gbM33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4820	17837	30735	3.62	4.2E-01	R13467.1	EST_HUMAN	yf77601.1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:28278 5'
5801	18883	32076	1.38	4.2E-01	BF242055.1	EST_HUMAN	601870721F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4108493 5'
5876	18865	32156	1.23	4.2E-01	AW854162.1	EST_HUMAN	RC3-C10254.060400-028-g04.C10254 Homo sapiens cDNA
6329	18936	32641	0.91	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7139	20715	33428	9.39	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7139	20715	33429	9.39	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7207	25677	33563	5.51	4.2E-01	S82504.1	NT	Breast breast cancer gene (rat), WF, spleen, Genomic, 419 nt, segment 2 of 2
7300	20272	33607	5.9	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7822	20770	34148	0.52	4.2E-01	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
8325	21294	34708	2.56	4.2E-01	AW957448.1	EST_HUMAN	EST389413 MAGE resequences, MAGE Homo sapiens cDNA
8325	21294	34709	2.56	4.2E-01	AW957448.1	EST_HUMAN	EST389413 MAGE resequences, MAGE Homo sapiens cDNA
8548	21518	34934	0.46	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
10329	23253		0.72	4.2E-01	AA705007.1	EST_HUMAN	Z65501.1st Soares_fetal_liver_spleen_INF1S S1 Homo sapiens cDNA clone IMAGE:482848 3'
10541	23493	36958	0.43	4.2E-01	AF161854.1	NT	Laesa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
10862	23782	37283	1.53	4.2E-01	AW963966.1	EST_HUMAN	MFR-SN0070-280300-103-107 SN0070 Homo sapiens cDNA
11382	24326	37658	2.39	4.2E-01	AB023489.1	NT	Oryzias latipes OIGG7 mRNA for membrane guanylyl cyclase, complete cds
11723	24809	38165	1.77	4.2E-01	BE066485.2	EST_HUMAN	601860328F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906385 3'
13080	25616		1.4	4.2E-01	AL392837.1	EST_HUMAN	lg1805.51 NC1_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108360 3'
1098	14140	27090	1.98	4.1E-01	AB095481.1	EST_HUMAN	RC-B11091-210198-142 B11091 Homo sapiens cDNA
1105	14149	27096	1.33	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADS Homo sapiens cDNA clone ADBAHF08 5'
1105	14149	27100	1.33	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADS Homo sapiens cDNA clone ADBAHF08 5'
2722	15716	28734	1.43	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2951	16008	28652	2.07	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2951	16008	28652	2.07	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3314	16367	29287	0.89	4.1E-01	AA906344.1	EST_HUMAN	g94b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1605943 3'
4303	17332	30212	2.54	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoA, isoB, isoC, isoD, isoE and isoF genes
4334	17382		0.84	4.1E-01	AA909257.1	EST_HUMAN	om33402.1st Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4694	17715	30610	1.71	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NP25DF10 5'
6103	19182	32401	4.57	4.1E-01	BF681363.1	EST_HUMAN	6027156590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
6877	19930	33227	0.58	4.1E-01	U02268.1	NT	Mus musculus NIH 3T3 chondroblastic rat (Soyas) gene, complete cds
7668	20025	33989	2.96	4.1E-01	U671535.1	NT	Melanimococcus jamaicensis section 77 of 150 of the complete genome
8370	21339	34750	1.16	4.1E-01	BF574804.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4286238 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9445	22409	35946	1.46	4.1E-01	8755521	NT	Mus musculus signaling intermediate in Toll pathway evolutionarily conserved (Slpsec-pending), mRNA
8923	22807		0.98	4.1E-01	AF160597.1	NT	Volevo gymnocaudus Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
10626	23548		1.18	4.1E-01	AL138076.2	NT	Campylobacter jejuni NCCTC11168 complete genome, segment 3/6
10775	23598	37764	1.1	4.1E-01	AV649579	EST_HUMAN	AV649579 GLC Homo sapiens cDNA clone GLC5D12.3
10873	23763	37294	0.91	4.1E-01	P18594	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10873	23763	37295	0.91	4.1E-01	P18594	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10943	23863		2.1	4.1E-01	BF346382.1	EST_HUMAN	CM2-HT0137-2003988-010-e08 HT0137 Homo sapiens cDNA
11188	24144	37677	39.55	4.1E-01	X56700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zein protein
12781	26931		3	4.1E-01	087675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
142	15833		0.65	4.0E-01	AW/847123.1	EST_HUMAN	RC2-CT0201-280998-012-010 CT0201 Homo sapiens cDNA
1040	14085	27036	0.71	4.0E-01	8404656	NT	Laqueus rubellus mitochondrion, complete genome
1342	14377	27346	1.17	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dm) mRNA, complete cds
1481	14514		5.11	4.0E-01	6879258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2022	16883	28054	1.12	4.0E-01	Z66933.1	NT	Aerobolus immitis mas2 gene
2022	16883	28056	1.12	4.0E-01	Z66933.1	NT	Aerobolus immitis mas2 gene
2167	15183	28203	1.09	4.0E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2167	15183	28204	1.09	4.0E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2816	13246	26176	1.27	4.0E-01	6678480	NT	Mus musculus ubiquitin-protein ligase e3 component h-recogin (Ubr1), mRNA
2878	16037	28959	1.34	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2978	16037	28960	1.34	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3708	16752	29668	2.32	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae Y1C (MIC), Y1D (MID), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3840	16880	29783	3.28	4.0E-01	AI277511.1	NT	Ovis aries partial J22 gene for T cell receptor delta chain (TCRDJ2), exon 1
3840	16880	29784	3.28	4.0E-01	AI277511.1	NT	Ovis aries partial J22 gene for T cell receptor delta chain (TCRDJ2), exon 1
4855	17872		9.36	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
5015	19068	32299	1.14	4.0E-01	AW570610.1	EST_HUMAN	EST1382891 IMAGE:resquences, MAGK Homo sapiens cDNA
6226	19300	32533	0.51	4.0E-01	BF243741.1	EST_HUMAN	60187/6183F/NIH_MGC_55 Homo sapiens cDNA clone IMAGE:106221.5
6578	19638	32804	0.92	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 8 KD PEPTIDE]
8345	21314	34729	0.8	4.0E-01	AB018625.1	NT	Homo sapiens OCTN2 gene, complete cds
8350	22325	35753	0.88	4.0E-01	AA322289.1	EST_HUMAN	EST125066 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11895	24776		2	4.0E-01	BF030262.1	EST_HUMAN	601562832F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5'
12030	24906		1.75	4.0E-01	L76080.1	NT	Synecocystis sp. PCC 6413 transposase gene, complete cds
12448	25763		3.03	4.0E-01	AL163500.2	NT	Homo sapiens chromosome 21 segment HS21G100
12968	25538		1.6	4.0E-01	P36049	SWISSPROT	HYPOPHOSPHATASE 1 KD PROTEIN IN GINGIVITIS INTERGENIC REGION
1378	14412	27383	1.85	3.9E-01	AF206518.1	NT	Goatella gorilla carboxyl-ester lipase (CEL) gene, complete cds
2650	15647	28670	3.82	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1192 protein, partial cds
2716	15710	28726	4.26	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2718	15710	28727	4.26	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3113	16170	29080	4.56	3.9E-01	AJ226866.1	NT	Shorthorn-bloom meliloti egf, syb2, cys3 genes and ori3
4105	17140	30035	1.25	3.9E-01	BF526811.1	EST_HUMAN	7161d01.x1 NCI CGAP B16 Homo sapiens cDNA clone IMAGE:3339189 3'
5027	18041	30824	1.74	3.9E-01	BE726657.1	EST_HUMAN	601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833099 5'
6042	19124	32329	5.85	3.9E-01	BF280336.1	EST_HUMAN	601862382F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6411	19479	32726					Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8266	121255	34694	0.6	3.9E-01	U76415.1	NT	Homo sapiens prepro dipeptidyl peptidase 1 (DPP-I) gene, complete cds
9213	22179	35610	0.73	3.9E-01	AW177011.1	EST_HUMAN	GM3-CT0105-170899-004-b08 CT0105 Homo sapiens cDNA
9222	22188		0.68	3.9E-01	BF346934.1	EST_HUMAN	602016944F1 NCI CGAP B167 Homo sapiens cDNA clone IMAGE:4155322 5'
9580	22552	36003	1.41	3.9E-01	AW185888.1	EST_HUMAN	x88d04.x1 Sores_NFL_T_OBC_51 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR-094821
9903	22655	38316	1.83	3.9E-01	AJ937337.1	EST_HUMAN	094821 KIAA0713 PROTEIN
10237	23162	36650	2.89	3.9E-01	M16879.1	NT	SW-RFX5 HUMAN P48382 BINDING REGULATORY FACTOR.1
10305	23230		0.48	3.9E-01	11465820	NT	Human tubulin 27 gene, exons 10 and 11, and L1 and A1 repeats
10527	23449	36947	0.62	3.9E-01	D86722.1	NT	Porphyra purpurea mitochondrion, complete genome
10665	23885	37397	0.48	3.9E-01	M18440.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
12219	25668		4.08	3.9E-01	AF304354.1	NT	Human beta-B2-crystallin (B2-1) gene, exon 4, partial cds
12344	25142		2.01	3.9E-01	Q51670	SWISSPROT	Homo sapiens proteolipican 3 (PRC3) gene, complete cds
12840	25452		1.49	3.9E-01	11433335	NT	HOMEOBOX PROTEIN HLX1
161	13264		9.02	3.8E-01	7019468	NT	Homo sapiens hypothetical protein FL10688 (FL10688), mRNA
506	13577		0.8	3.8E-01	AB029291.1	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1686	14911		1.19	3.8E-01	AE003870.1	NT	Mus musculus pcrn-1 mRNA for pericentriolar material-1, complete cds
2465	15469	28493	1.24	3.8E-01	U41846.1	NT	Xkallia fastidiosa, scopolin, 16 of 226 of the complete genome
2577	15578	28597	2.26	3.8E-01	AF214117.1	NT	Oenothera biennis trigonase acetylcholinesterase (ace-1) gene, complete cds
							Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2640	15900	26682	4.89	3.8E-01	6678002	NT	Mus musculus soluble carrier family 1, member 6 (Sic1a6), mRNA
3015	16073		0.88	3.8E-01	AJ251067.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3061	16118	29033	0.93	3.8E-01	AF043383.1	NT	Pleuroctenaeus americanus aminopeptidase N (amphN) gene, partial cds
3495	16542	29466	9.24	3.8E-01	AL191518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3549	16595		0.75	3.8E-01	AI807218.1	EST_HUMAN	w33812.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855.3'
3666	16655		0.97	3.8E-01	AI807218.1	EST_HUMAN	w33812.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855.3'
3769	16811	29720	0.89	3.8E-01	BE154080.1	EST_HUMAN	PMO-HT0339-200-400-070-G01 HT0339 Homo sapiens cDNA
5691	18786	31967	1.08	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6473	19538		0.6	3.8E-01	S46825.1	NT	p10n protein [milk, Genomic, 2446 nt]
6779	19834	33117	5.49	3.8E-01	BE072399.1	EST_HUMAN	QV3-B1T0537-271299-049-e02 B1T0537 Homo sapiens cDNA
6924	20148	33468	4.76	3.8E-01	AI374601.1	EST_HUMAN	t65411.x1 Soares_fetal_Nb2HP9_9w Homo sapiens cDNA clone IMAGE:2047917.3' similar to contains Alu repetitive element;
7126	20059	33365	1.24	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7743	20697	34063	0.61	3.8E-01	AA626274.1	EST_HUMAN	zu88c05.s1 Soares_testis NIH Homo sapiens cDNA clone IMAGE:745084.3'
7759	20712		4.27	3.8E-01	X61597.1	NT	Mus musculus gene for tallitric-binding protein
7988	20937	34331	0.49	3.8E-01	V00683.1	NT	Yeast mitochondrial gene for ATPase (genes oil-2 and oil-4)
8640	21608	35031	0.45	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8903	21869	35294	2.04	3.8E-01	AB046951.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8972	21938	35363	0.79	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9169	22135	35561	1.47	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9819	22740		6.02	3.8E-01	TB5413.1	EST_HUMAN	y64306.11 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:120539.5' similar to contains Alu repetitive element; contains PFRS repetitive element;
11862	24744		3.41	3.8E-01	BE178216.1	EST_HUMAN	RCO-HT0841-04080-032-b12 HT0841 Homo sapiens cDNA
12000	24871	38473	2.61	3.8E-01	R42550.1	EST_HUMAN	y62811.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:30289.3'
12000	24871	38474	2.61	3.8E-01	R42550.1	EST_HUMAN	y62811.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:30289.3'
12433	25199		4.23	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12557	25689		2.63	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12687	25343		2.84	3.8E-01	BE29256.1	EST_HUMAN	QV3-ET0083-190700-271-a05 ET0083 Homo sapiens cDNA
13056	25644		2.03	3.8E-01	AF281483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1tra4) gene, complete cds
13063	25905		1.4	3.8E-01	T54787.1	EST_HUMAN	y42811.s1 Stratiopene fetal spleen (8937205) Homo sapiens cDNA clone IMAGE:73821.3' similar to similar to dbA06977 SERJUN ALBUMIN PRECURSOR (HUMAN)
13080	26611	31690	1.57	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2490	15493	28518	12.56	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3474	16520	29442	11.71	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3884	16924	28833	0.7	3.7E-01	AA319482.1	EST_HUMAN	EST121715 Adrenal gland tumor Homo sapiens cDNA 5' and
4257	17286	30168	6.92	3.7E-01	AI218707.1	EST_HUMAN	033607.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1610188 3'
4348	17375	30255	1.64	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-002 OT0007 Homo sapiens cDNA
4416	17443	30334	3	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 205 of the complete genome
5857	18847	32132	1.16	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6050	19141	32355	1.35	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6659	18716	32963	0.96	3.7E-01	M10806.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6980	18737	32963	0.77	3.7E-01	L10353.1	NT	Mus musculus hemoglobin mRNA, complete cds
7350	20320	33657	3.48	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7658	20618	33983	0.65	3.7E-01	BE873743.1	EST_HUMAN	601483897F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
7658	20618	33984	0.95	3.7E-01	BE873743.1	EST_HUMAN	601483897F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
8069	21005	34404	0.71	3.7E-01	166802.1	EST_HUMAN	y650d7.r3 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:96324 5'
8672	21640	35084	1.93	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8672	21640	35065	1.93	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8708	21678	35101	0.69	3.7E-01	AA902912.1	EST_HUMAN	0443b11.s1 NCI_CGAP_Led2 Homo sapiens cDNA clone IMAGE:1516701 3'
8556	22513		3.78	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (BCDO gene)
10530	23452		0.52	3.7E-01	K00691.1	NT	mouse Ig germline alpha membrane exons region
10570	23492	36984	3.95	3.7E-01	A1336411.1	EST_HUMAN	q14607.x1 Soares_fetal_Jung_NIH-L16W Homo sapiens cDNA clone IMAGE:1950697 3'
11205	24159	37689	1.9	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
11369	24316	37842	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens perlecan LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11369	24316	37843	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens perlecan LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11794	23849	37470	2.34	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (dT) (EC 2.7.7.31)
12014	24891		1.53	3.7E-01	AA873540.1	EST_HUMAN	0046003.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569221 3' similar to gb:U77698
12060	24833		3.22	3.7E-01	6677878	NT	TRANSSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
12136	25501		2.6	3.7E-01	J04982.1	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
12909	25177		4.23	3.7E-01	AJ24325.1	NT	Human heart/skeletal muscle A1P/ADP translocator (ANT1) gene, complete cds
12764	28406		1.86	3.7E-01	AL121154.1	EST_HUMAN	Chitanydophilin poliovirus partial omp1 gene for outer membrane protein 1
12829	25447	31722	2.71	3.7E-01	Y18000.1	NT	DKFZp762k075.1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZp762k075 5'
997	14048		11.36	3.6E-01	U89241.1	NT	Homo sapiens NF2 gene
1317	14352	27320	2.66	3.6E-01	T80255.1	EST_HUMAN	Human m14g gene, partial cds
1317	14352	27321	2.66	3.6E-01	T80255.1	EST_HUMAN	y03a05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1317	14352	27321	2.66	3.6E-01	T80255.1	EST_HUMAN	y03a05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1831	14955	27951	6.09	3.6E-01	AW560184.1	EST_HUMAN	h338102.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947419 3'
1831	14955	27952	6.09	3.6E-01	AW560184.1	EST_HUMAN	h338102.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947419 3'

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit: Descriptor
1968	14389	27992	6.4	3.8E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2399	16408		3.58	3.8E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2483	15487	28510	1.29	3.8E-01	U05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2483	15487	28511	1.29	3.8E-01	U05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2495	15498	28524	1.63	3.8E-01	AW812633.1	EST_HUMAN	RCS-ST0171-181099-001-1-007 ST0171 Homo sapiens cDNA
2638	15637	28660	1.23	3.8E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE)
2910	18322		5.89	3.8E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3483	16529	29453	2.01	3.8E-01	X76758.1	NT	H. sapiens serotoninn transporter gene, exons 9 and 10
3483	16529	29454	2.01	3.8E-01	X76758.1	NT	H. sapiens serotoninn transporter gene, exons 9 and 10
4438	17482	30351	1.14	3.8E-01	BE707883.1	EST_HUMAN	RCT-HT0545-19680-014-612 HT0545 Homo sapiens cDNA
4787	17805	30697	0.72	3.8E-01	Y11526.1	NT	Zmays mRNA for casein kinase II alpha subunit
5045	18058	30937	2.81	3.8E-01	AW339393.1	EST_HUMAN	hnd2p04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5136	18145	31025	0.65	3.8E-01	BE067699.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0359 Homo sapiens cDNA
5274	18280	31143	0.91	3.8E-01	AF067958.1	NT	Gallus gallus homocodomin protein HOXD-3 mRNA, complete cds
5274	18280	31144	0.91	3.8E-01	AF067958.1	NT	Gallus gallus homocodomin protein HOXD-3 mRNA, complete cds
5456	18558	31469	0.71	3.8E-01	AJ006505.1	NT	Homo sapiens lipo gene Intron 5
6205	19279	32512	1.1	3.8E-01	P18431	SWISSPROT	FORMAT HYDROGENYLASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6822	19881	32958	1.8	3.8E-01	Y10195.1	NT	Homo sapiens PHEX gene
7355	20325		3.63	3.8E-01	R94890.1	EST_HUMAN	X74406.r1 Soares fetal liver apc1c1 1NfLS Homo sapiens cDNA clone IMAGE:275887 5'
7500	20465	33826	1.86	3.8E-01	AW027174.1	EST_HUMAN	w72c10.x1 Soares_lhynus_JNHfTh Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR-O15117
8568	21534	34954	0.64	3.8E-01	P98167	SWISSPROT	O15117 PYN BINDING PROTEIN. [1];
8622	21590	35008	14.05	3.8E-01	AL161583.2	NT	SCO SPONDIN
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
9330	22285	35724	0.53	3.8E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9330	22295	35725	0.53	3.8E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9355	22320	35748	2.84	3.8E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9355	23230	35747	2.84	3.8E-01	4504958	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9547	22510	35959	1.12	3.8E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9754	22695	36151	0.93	3.8E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9754	22695	36152	0.93	3.8E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9824	22873	36638	0.54	3.8E-01	X62825.1	NT	C. perficiens plc gene for phospholipase C upstream region containing bent DNA fragment
10222	23147	36638	19.06	3.8E-01	Q33194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y41S
10352	23276	36750	0.48	3.8E-01	AW752801.1	EST_HUMAN	MR2-CT10222-211095-002-b10 CT10222 Homo sapiens cDNA
10352	23276	36751	0.48	3.8E-01	AW752801.1	EST_HUMAN	MR2-CT10222-211095-002-b10 CT10222 Homo sapiens cDNA
11292	24242	37769	3.04	3.8E-01	BE902390.1	EST_HUMAN	601678418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3968897 5'
11442	24385	37925	3.26	3.8E-01	AB004233.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11772	23927	37448	5.83	3.8E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
12174	25989		2.05	3.8E-01	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exon 1 to 9
12247	25076		1.42	3.8E-01	D96901.1	NT	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
12257	25083		6.35	3.8E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 226 of 400 of the complete genome
12417	25187		6.26	3.8E-01	U68888.1	NT	Mus musculus Emr1 mRNA, complete cds
12770	25410		1.87	3.8E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) (Drosophila) homolog); translocated to 10 (AF10), mRNA
13033	25834		3.33	3.8E-01	AW190228.1	EST_HUMAN	x60811.1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN)
115	13228	26150	1.42	3.5E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 36
210	13311	26238	3.29	3.5E-01	667863.3	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
728	13787	26722	1.48	3.8E-01	7706138	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
728	13787	26723	1.48	3.5E-01	7706138	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
750	13840	26785	4.95	3.5E-01	BF126798.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4063851 3'
1623	14656	27634	0.99	3.5E-01	BF310388.1	EST_HUMAN	601844553F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1646	14678	27651	2.57	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2281	15303	28528	1.28	3.5E-01	P06798	SWISSPROT	HOMEOBOX PROTEIN HOXA-4 (HOX-1.4) (MH-3)
2613	15899	28636	1.13	3.5E-01	AA223252.1	EST_HUMAN	z08a08.e1 Stralagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:950872 3'
3818	16858		7.27	3.5E-01	AA642138.1	EST_HUMAN	m60d03.s1 NCI CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4291	17320	30189	2.18	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb6) gene, complete cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4922	17939	30831	0.7	3.5E-01	N81203.1	EST_HUMAN	78BIE1 fetal brain cDNA Homo sapiens cDNA clone 78BIE1-K similar to R07879, 240488
4969	17984	30874	6.46	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5407	18510	31387	0.84	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5407	18510	31388	0.84	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5629	18725	31886	1.36	3.5E-01	D42045.1	NT	Human mRNA for KIAA0088 gene, complete cds
6365	19434		0.77	3.5E-01	AW863916.1	EST_HUMAN	PMA-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA
6548	19609	32671		3.5E-01	AA431833.1	EST_HUMAN	zw78003.r1 Scanes, testis, NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR/G1068935
6593	19653	32525	0.88	3.5E-01	U37160.1	NT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
6821	19875	33164	0.92	3.5E-01	O24357	SWISSPROT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7287	19962		3.85	3.5E-01	X98505.1	NT	S. serotia mRNA for CD31 protein (PECAM-1)
7789	20742	34115	0.81	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7789	20742	34116	0.81	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8023	20660	34356	0.7	3.5E-01	X05091.1	NT	E. coli L-arabinose transport operon with genes araF, araG and araH
8406	21375		2.17	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8409	21378	34784	0.87	3.5E-01	BF358871.1	EST_HUMAN	RC4-E10024-260800-014-d07 E10024 Homo sapiens cDNA
8810	21777		0.58	3.5E-01	AF051561.1	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9279	22245	35674	1.14	3.5E-01	4507610	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
10083	23019	36464	6.84	3.5E-01	U02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOMER 5) (BRAIN CALCIUM CHANNEL III) (BII)
10246	23171	36660	5.61	3.5E-01	Z28825.1	NT	Xlaxis gene for albumin including HP1 enhancer
10328	23250	36729	1.01	3.5E-01	BE174794.1	EST_HUMAN	GV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
11086	24047	37569	2.48	3.5E-01	X61084.1	NT	C. carassius rhodopsin gene for opsin protein
11362	24311	37638	1.68	3.5E-01	AJ243178.1	NT	Gallus gallus SPARG gene for osteonectin, promoter and exon 1
11362	24311	37639	1.68	3.5E-01	AJ243178.1	NT	Gallus gallus SPARG gene for osteonectin, promoter and exon 1
11919	24800	38397	1.87	3.5E-01	N77597.1	EST_HUMAN	y980H12.r1 Scanes, multiple, sclerotic, 2NHHMSP Homo sapiens cDNA clone IMAGE:290375 5'
11940	24820		1.77	3.5E-01	M82685.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
11961	24868	38463	1.6	3.5E-01	U05146.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
12289	25691		1.8	3.5E-01	AF297468.1	NT	Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
12341	26139		1.31	3.5E-01	X84595.1	NT	B. taurus apA1 gene for F0(J)1 ATP synthase alpha-subunit
12501	25240		2.96	3.5E-01	AE001774.1	NT	Thermoplasma maritima section 86 of 136 of the complete genome
13085	25842	31430	3.37	3.5E-01	H80814.1	EST_HUMAN	y64411.r1 Scanes retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
13085	25842	31431	3.37	3.5E-01	H80814.1	EST_HUMAN	y64411.r1 Scanes retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13108	25627		1.97	3.9E-01	4758297	NT	Homo sapiens w-hb2, avian erythroblastic leukemia viral oncogene homolog 2 (neuroglobin) derived oncogene homolog (ERBB2), mRNA
708	13770		1.97	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
977	14028	26982	9.08	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, cds genes, crf22 and partial inaA gene
1329	14364	27332	2.78	3.4E-01	Y00554.1	NT	Azobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2410	15417	28441	2.01	3.4E-01	D90609.1	NT	Synedococcus sp. PCC6803 complete genome, 11/27, 1311235-1430418
3014	16072	28982	0.98	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3014	16072	28983	0.98	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3175	16230	29146	6.62	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3354	16405	29328	0.94	3.4E-01	AF034652.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3542	16588	29512	3.42	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SST putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3804	16844		1.78	3.4E-01	BF440010.1	EST_HUMAN	7n84e01.x1 NC1 CGAP_Ox18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8UJ15
4082	17116		1.48	3.4E-01	AA584196.1	EST_HUMAN	Q9UJ15.DJ1809.1
4874	17695	30582	1.72	3.4E-01	BE069912.1	EST_HUMAN	nc01b10.g1 NC1 CGAP_Phat Homo sapiens cDNA clone IMAGE:1100347 3'
4989	18004		4.71	3.4E-01	AI240753.1	EST_HUMAN	WRA-BT0403-230200-202-001 BT0403 Homo sapiens cDNA
5769	18950	32040	2.74	3.4E-01	AL161594.2	NT	q95605.x1 NC1 CGAP_X103 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains A11 repetitive element
5909	18995		5.14	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6122	19200		1.74	3.4E-01	L02971.1	NT	zn12d11.11 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3'
6146	19221	32451	0.8	3.4E-01	BE748912.1	EST_HUMAN	Echovirus 22 TAB_1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6229	19303	32535	1.91	3.4E-01	AW204505.1	EST_HUMAN	601571811T1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3638826 3'
6362	19431	32674	1.78	3.4E-01	AL120544.1	EST_HUMAN	U1-H-B11-es-6-12-0-U1e1 NC1 CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6907	19569		1.19	3.4E-01	N65225.1	EST_HUMAN	DKFZ761A249.t1 T61 (synonym: barmy2) Homo sapiens cDNA clone DKFZ761A249.5'
7135	20111	33424	1.14	3.4E-01	AI468082.1	EST_HUMAN	2459a.12.31 Series, fetal lung_NHL19W Homo sapiens cDNA clone IMAGE:307342 3'
7261	19995	33293	0.91	3.4E-01	BF678702.1	EST_HUMAN	118595.x1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2182840 3' similar to gb:537431
8238	21207		0.64	3.4E-01	AE000463.1	NT	LAMININ RECEPTOR (HUMAN);
8579	21547	34866	0.95	3.4E-01	Y14600.1	NT	602085233F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248365 5'
8832	21769		1.8	3.4E-01	AA337083.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 383 of 400 of five complete genome
							Homo sapiens TCRA/28 gene, allele A4, partial
							EST147165 Chromosomal tumor Homo sapiens cDNA 5' end

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8909	21875	35301	0.84	3.4E-01	L04890.1	NT	Citriculus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
9204	22170	35900	1.89	3.4E-01	9633924	NT	Bovine enterovirus strain K2577, complete genome
9507	22529	35978	4.43	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9587	22628	35979	4.43	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9776	22717		0.49	3.4E-01	AB017510.1	NT	Epithelial tumellitis mRNA for PLO-gammaS, complete cds
9801	21124	34527	6.03	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Marf1 (MAF1) gene, complete cds
9801	21124	34528	6.03	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Marf1 (MAF1) gene, complete cds
9855	22761	36243	0.43	3.4E-01	AF163857.1	NT	Dichostemum discoidium putative CMF receptor CMFR1 mRNA, complete cds
10354	22951	36449	1.09	3.4E-01	U89763.1	NT	Glycine max putative transcription factor SCOF-1 (scsf-1) mRNA, complete cds
10249	23174	36654	2.14	3.4E-01	AJ225084.1	NT	Homo sapiens FAX gene, exon 16, 17 and 18
10843	23763		0.88	3.4E-01	AED00496.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
11357	24307		3.51	3.4E-01	AED00389.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
11393	24339	37869	4.96	3.4E-01	P08925	SWISSPROT	PROBABLE EA PROTEIN
11427	24371	37909	1.67	3.4E-01	AF045981.1	NT	Rattus serali cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11828	24711	38295	1.58	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-gliadin/MUC18, complete cds
11856	24738	38323	3.3	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12069	24970	38567	1.9	3.4E-01	AJ559986.1	EST_HUMAN	h7706.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE2214874 3' similar to contains L1.b1 L1 repetitive element;
12149	25008		2.08	3.4E-01	U89604.1	NT	Citrus variegation virus putative replicase gene, partial cds
12261	25085		1.59	3.4E-01	Z21621.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
12485	25231		13.04	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
12512	25761		3.88	3.4E-01	BE216852.1	EST_HUMAN	h42109.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE3176127 3' similar to contains PTR5.B3 PTR5 repetitive element;
12567	25805		2.19	3.4E-01	9838391	NT	Beta vulgaris mitochondrion, complete genome
12673	25845	31763	3.46	3.4E-01	AJ297131.1	NT	Mus musculus SLL MAP_17_CYP_a, SCL & CYP_b genes
12872	25838		1.94	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK2W), RD, complement factor B (B), and complement component C2 (C2) genes;>
151	13135	26033	10.37	3.3E-01	X07690.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
100	13135	26033	4.34	3.3E-01	X07690.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
448	13521	26454	1.3	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
534	13700	26821	2.26	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1205	14244	27203	3.29	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1310	14346	27312	2.44	3.3E-01	BF568880.1	EST_HUMAN	602184016T1 NIH MGC_42 Homo sapiens cDNA clone IMAGE:4300261 3'
1610	14642	27618	1.55	3.3E-01	8753085	NT	Mus musculus desintegrin 5 (Dign5), mRNA
1752	14781		1.13	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2043	15062		1.01	3.3E-01	AF031148.1	NT	Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
2414	15421		4.45	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (uridine phosphorylase transferase and oridine 5'-decarboxylase) (UMPS) mRNA
2660	16018	26945	1.76	3.3E-01	AJ251805.1	NT	Bacteriophage phi-Y6C3-12 complete genome
3028	19086		0.8	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3058	18125	29038	0.91	3.3E-01	AJ007932.2	NT	Streptomyces griseolus mltiramylin biosynthetic genes
3506	16553	29479	1.27	3.3E-01	A8012922.1	NT	Homo sapiens MTA14-1 gene, complete cds
3822	16822	29766	2.18	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3832	16872	29773	0.8	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3989	17020	29639	1.54	3.3E-01	AL181498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4026	17064	29665	2.02	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4395	17423		1.51	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for neupilin, partial cds
4715	17793		1.41	3.3E-01	A1539114.1	EST_HUMAN	187812.x1 NCL_GCAP_UB Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN)
4875	17692	30781	1.33	3.3E-01	D64003.1	NT	Synchytrium sp. PC68003 complete genome, 22/27, 2755703-2888766
5397	18500	31377	2.48	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3UTR of ubiquitin-like protein
5397	18500	31378	2.48	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3UTR of ubiquitin-like protein
5684	18759	31928	0.55	3.3E-01	P36055	SWISSPROT	DYNAMIN
5684	18759	31929	0.55	3.3E-01	P36055	SWISSPROT	DYNAMIN
5684	18759	32166	0.61	3.3E-01	BF213873.1	EST_HUMAN	601846090F1 NIH MGC_58 Homo sapiens cDNA clone IMAGE:4078823 5'
5684	18759	32167	0.61	3.3E-01	BF213873.1	EST_HUMAN	601472768T1 NIH MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6056	19137	32347	1.75	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6056	19137	32348	1.75	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6154	19229	32489	0.82	3.3E-01	P05691	SWISSPROT	CIRCUMFORZOTE PROTEIN (CS)
6590	20185	33508	0.63	3.3E-01	AB034233.1	NT	Flexibacter litorealis gyrB gene for DNA gyrase B subunit, partial cds
6590	20185	33509	0.63	3.3E-01	AB034233.1	NT	Flexibacter litorealis gyrB gene for DNA gyrase B subunit, partial cds
7073	20095	33404	4.16	3.3E-01	A1028131.1	EST_HUMAN	194401.x1 NCL_GCAP_Kid11 Homo sapiens cDNA clone IMAGE:2295809 3' similar to contains Alu repetitive element/contains element L1 repetitive element;



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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7073	20095	33405	4.16	3.3E-01	AB28131.1	EST_HUMAN	h6101.x1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains A1u repetitive element contains element L1 repetitive element;
8062	20898	34395	1.81	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8908	21874	35300	22.63	3.3E-01	BF683954.1	EST_HUMAN	602710372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
9080	22046	35469	0.96	3.3E-01	BF210322.1	EST_HUMAN	601973281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4087180 5'
9469	22433	35871	0.85	3.3E-01	Q82625	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9733	22761	36215	0.98	3.3E-01	BE828491.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9733	22761	36216	0.98	3.3E-01	BE828491.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9859	22905	36258	2.8	3.3E-01	N68866.1	EST_HUMAN	z66701.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:287649 3'
9910	22731	36186	2.51	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
10350	23274		2.12	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGB-C) gene, exons 1-3, complete cds
11076	24038	37561	2.85	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
11078	24038	37562	2.85	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
11365	24313		2.16	3.3E-01	BF526499.1	EST_HUMAN	h611g02.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
11565	24505	38082	8.16	3.3E-01	BE218351.1	EST_HUMAN	GALACTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
11673	24639	38218	3.19	3.3E-01	P47953	SWISSPROT	
12027	24903		3.43	3.3E-01	AA80621.1	EST_HUMAN	Rhizobium leguminosarum ssp. phaseolus PRL5J1 nodX gene
12044	13135	26033	1.97	3.3E-01	X07960.1	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
12248	25075	38170	1.84	3.3E-01	6598319	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (2/7)
12668	25630	31621	4.82	3.3E-01	AP000002.1	NT	601146730F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162006 5'
13113	25932		1.59	3.3E-01	BE312920.1	EST_HUMAN	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
457	13530		2.08	3.3E-01	AF018261.1	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 61
719	13781		0.76	3.2E-01	AL161561.2	NT	5' upstream ppsv virus T RNA2 putative RNA dependent RNA polymerase gene, complete cds
1166	14207	27161	10.6	3.2E-01	AF047013.1	NT	P. vulgaris arch-1 gene
1287	14522	27265	1.77	3.2E-01	Z50202.1	NT	
1301	14425	27394	5.96	3.2E-01	Q49624	SWISSPROT	LAGCTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1839	14671		0.9	3.2E-01	AF209730.1	NT	Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds
1789	14818	27803	1.5	3.2E-01	Z36041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1799	14828	27815	5.47	3.2E-01	AW657194.1	EST_HUMAN	EST1369264 VAGE resequences, NAGO Homo sapiens cDNA
1799	14828	27816	5.47	3.2E-01	AW657194.1	EST_HUMAN	EST1369264 VAGE resequences, NAGO Homo sapiens cDNA

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1800	14886	27882	1.03	3.2E-01	AL111656.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2168	15184	28205	2.33	3.2E-01	BF203817.1	EST_HUMAN	60186804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2548	15549		2.3	3.2E-01	7710078	NT	Mus musculus Pdx1-related 1 homeobox (Pbx1), mRNA
2720	15714	28732	1.98	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3322	16665		0.79	3.2E-01	D10872.1	NT	Human 1 NAT allele 3-2 gene for arylamine N-acetyltransferase
4367	17394	30273	0.63	3.2E-01	4759195	NT	Homo sapiens myelinin (SYM) mRNA
4422	17449	30340	1.62	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4526	17651	30439	1.3	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL_81.7 KD PROTEIN CT337.04C IN CHROMOSOME 1 PRECURSOR
4767	17787		8.32	3.2E-01	BF693817.1	EST_HUMAN	60208197Z1F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4915	17932	30823	0.69	3.2E-01	Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY
5250	18268	31127	0.96	3.2E-01	AY008847.1	NT	PROTEIN 3) ACCESSORY ADHESIN PROTEIN 3) (P69)
5280	18298		4.18	3.2E-01	A1969472.1	EST_HUMAN	Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5344	18449	31320	2.71	3.2E-01	BE173964.1	EST_HUMAN	repetitive element/contains dement PTR7 repetitive element ;
6068	19149	32361	1.36	3.2E-01	L27221.1	NT	CMC-H10569-060300-289-110 HT0569 Homo sapiens cDNA
6436	19802	32753					Giardia intestinalis pyruvate:ferredoxin oxidoreductase and flanking genes
6749	19803	33084	0.68	3.2E-01	AF016494.1	NT	Fugu ribophis gamma-aminobutyric acid receptor beta subunit gene, partial cds, 55kd erythrocyte membrane
6897	19849		0.91	3.2E-01	AV718037.1	EST_HUMAN	enhancer protein (PCCOCE) genes, complete c>
8183	21159	34598	1.03	3.2E-01	AB002359.1	NT	Human mRNA for KIA0361 gene, KIA0361 protein
8512	21460	34894	0.44	3.2E-01	AJ277861.1	NT	Human mRNA for KIA0361 gene, KIA0361 protein
8609	21577	34993	1.43	3.2E-01	M60268.1	NT	Homo sapiens partial LM01 gene for LM domain only 1 protein, exon 1
8710	21676	35103	0.45	3.2E-01	AJ231001.1	NT	Rat ISO-alpha trialfuric factor gene, complete cds
8713	21681	35108	18.12	3.2E-01	X02508.1	NT	Rattus norvegicus repeat, map NOS-D12Wax1
8805	21722		17.12	3.2E-01	BF511635.1	EST_HUMAN	H1 sapiens gene fragment for acetylcholine receptor (AChR), alpha subunit exons 8, 9 and 3' flanking region
8845	21812	35231	1.94	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8845	21812	35232	1.13	3.2E-01	BF246771.1	EST_HUMAN	60185550F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8919	21865	35311	1.13	3.2E-01	BF246771.1	EST_HUMAN	60185550F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
9019	21985	35405	2.13	3.2E-01	AE002016.1	NT	Deinococcus radiodurans R1 section 152 of 226 of the complete chromosome 1
9019	21985	35405	0.63	3.2E-01	U51028.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
9019	21985	35405	0.63	3.2E-01	U51028.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9422	22387	35826	0.49	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS210004
9432	22396		2.28	3.2E-01	MB6511.1	NT	Human monocytic antigen CD14 (CD14) mRNA, complete cds
9505	22468	35911	0.45	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9505	22468	35912	0.45	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10353	23277	36752	3.37	3.2E-01	U44914.1	NT	Borrelia burgdorferi p18mr2 cp32-2, erp2 and erpD genes, complete cds, and unknown genes
10559	23481	36876	0.5	3.2E-01	BE326230.1	EST_HUMAN	h46H08.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181569 3'
10674	23568		3.71	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
11028	23992	37519	3.03	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain. Striatum (cat3636206) Homo sapiens cDNA clone HFBD221
12286	25690		3.87	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12674	25943		1.39	3.2E-01	BE69846.1	EST_HUMAN	601607820.F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909532 5'
12804	25431		4.84	3.2E-01	Q83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12890	25719		1.48	3.2E-01	AF157625.1	NT	Bos taurus insulin-like growth factor receptor type I mRNA, complete cds
12938	25816		1.87	3.2E-01	L39874.1	NT	Homo sapiens doxycycline deaminase gene, complete cds
13001	25925	31305	1.33	3.2E-01	BE385776.1	EST_HUMAN	601275460.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2218954 3' similar to contains MER10.11
13108	25928	31646	1.38	3.2E-01	AI745111.1	EST_HUMAN	MER10 repetitive element;
2679	15975	28596	3.02	3.1E-01	R18951.1	EST_HUMAN	ye00100.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to
2708	15928	28717	4.64	3.1E-01	766197.1	NT	gib164241 QM PROTEIN (HUMAN)
2708	15928	28718	4.64	3.1E-01	766197.1	NT	Homo sapiens KIA00174 gene product (KIA00174), mRNA
2869	15929		1.63	3.1E-01	AW629036.1	EST_HUMAN	Homo sapiens KIA00174 gene product (KIA00174), mRNA
3188	16243		4.03	3.1E-01	AB029069.1	NT	h46H08.x1 NCJ_CGAP_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3927	16867	28680	0.83	3.1E-01	AI251586.1	NT	Mus musculus gene for Ser/Thr Kinase KKIAMRE, exon 6
4969	18014	30901	1.25	3.1E-01	AE003964.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5239	18247	31119	0.79	3.1E-01	AF130370.1	NT	Xylaria fastidiosa, section 130 of 229 of the complete genome
5297	18320	31162	2.59	3.1E-01	AF163203.2	NT	Rattus norvegicus MEN1 tumor suppressor (Men1) mRNA, alternative splice product, complete cds
5555	18552	31596	9.76	3.1E-01	AF176111.1	NT	Homo sapiens chromosome 21 segment HS210003
5981	18775	31948	0.85	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5981	18777	31949	0.87	3.1E-01	P44132	SWISSPROT	HYPOPHYSICAL PROTEIN H1236
5982	18778	31949	0.87	3.1E-01	P274883.1	NT	HYPOPHYSICAL PROTEIN H1236
5983	18786		1.01	3.1E-01	Y13278.1	NT	Saccharomyces cerevisiae chromosome XV reading frame ORF YOL141W
5983	18786		1.01	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5986	18955	32142	2.3	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6416	29680	32732	0.61	3.1E-01	R64222.1	EST_HUMAN	y44104.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:198367 5'
6610	19688	32944	2.69	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-004 HN0001 Homo sapiens cDNA
6683	19740	33015	0.85	3.1E-01	A1264458.1	EST_HUMAN	q93401.x1 NCL_CGAP_CoR Homo sapiens cDNA clone IMAGE:1674689 3'
6840	18888	33188	0.88	3.1E-01	X771887.1	NT	H.sapiens gene for Immunoglobulin kappa light chain variable region A8 and A9
6850	20154	33288	0.7	3.1E-01	AW377354.1	EST_HUMAN	MR2-CT0222-281099-003-005 CT0222 Homo sapiens cDNA
7162	26634	34278	2.55	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7942	20884	34288	0.56	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8038	20975	34371	0.49	3.1E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 8 (Naipe) gene, complete cds, and Naipe3 gene, exons 2-9 and 11-16
8168	21104	34502	0.54	3.1E-01	AW950168.1	EST_HUMAN	IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA
8166	21104	34503	0.54	3.1E-01	AW950168.1	EST_HUMAN	IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA
8895	21961	35386	0.83	3.1E-01	RA5318.1	EST_HUMAN	y94801.x1 Soares infant brain 1NB Homo sapiens cDNA clone IMAGE:35639 3'
10282	23187	36671	0.52	3.1E-01	6876922	NT	Mus musculus p38alpha/tyrosine-4-phosphate 5-kinase, type 1 gamma (Pip3k1c), mRNA
10427	23349	36833	1	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
10427	23349	36834	1	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
10488	23410	36907	1.73	3.1E-01	A1244001.1	EST_HUMAN	q81611.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1983980 3' similar to gb:555700
10666	23588		0.56	3.1E-01	T55325.1	EST_HUMAN	HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
11186	24142	37676	2.35	3.1E-01	BF216117.1	EST_HUMAN	y94708.x1 Stratigene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74387 3' similar to similar to gb:M91036_m22 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
11864	24746	38328	2.3	3.1E-01	7682281	NT	601883502F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4088814 5'
12133	25002	38608	1.68	3.1E-01	AF048693.1	NT	Homo sapiens KIA00764 gene product (KIA00764), mRNA
12133	25002	38609	1.68	3.1E-01	AF048693.1	NT	Homo sapiens KIA00764 gene product (KIA00764), mRNA
12415	25186		1.57	3.1E-01	AF294308.1	NT	Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
12451	25210		4.84	3.1E-01	AF304162.1	NT	Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
12592	25296		4.19	3.1E-01	AF195953.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12944	25523		3.39	3.1E-01	AF196779.1	NT	Silvestroia vitreum 40S ribosomal protein S11 mRNA, partial cds
73	19508	28112	1.78	3.0E-01	6755083	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
264	13351	26277	8.98	3.0E-01	AJ271735.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds; and L-type calcium channel 2p
1227	14265	27222	2.16	3.0E-01	AW300400.1	EST_HUMAN	Mus musculus protein kinase C, epsilon (Pkcε), mRNA
1508	14541	27512	5.96	3.0E-01	AJ008755.1	NT	Homo sapiens X4 pseudobulbar region, segment 1/2
							x638108.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
							Balanoptera physalus gene encoding atrial natriuretic peptide

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2146	15162	28178	1.13	3.0E-01	AF237778.1	NT	Rattus norvegicus Cuz2/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3225	18280		1.28	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 eiyfG gene for polyketonate lyase, complete cds
3879	16918	29827	1.46	3.0E-01	AW817785.1	EST_HUMAN	PMA-ST0262-261199-001-001 ST0262 Homo sapiens cDNA
3998	17037	29944	1.02	3.0E-01	AJ271738.1	NT	Homo sapiens Xa pseudobulbosomal region; segment 2/2
4541	17564	30451	2.17	3.0E-01	AJ006755.1	NT	Balenoptera physalus gene encoding atrial natriuretic peptide
5425	18528	31407	5.19	3.0E-01	BE741629.1	EST_HUMAN	6015949501 NIH_MGC_9 Homo sapiens cDNA clone IMAGE3948734 5'
5506	18006	31536	0.56	3.0E-01	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
5510	18910	31541	0.78	3.0E-01	AF22627.1	NT	Canis lupus familiaris hemagglutinin gene, complete cds
5592	18978	31641	3.81	3.0E-01	BE693575.1	EST_HUMAN	RC9-BT0333-180700-111-003 BT0333 Homo sapiens cDNA
5592	18978	31642	3.81	3.0E-01	BE693575.1	EST_HUMAN	RC9-BT0333-180700-111-003 BT0333 Homo sapiens cDNA
5619	18715	31874	4.05	3.0E-01	U01247.1	NT	Mus musculus 1.29/kv Clara cell 10 kd protein (mCC10) gene, complete cds
7035	20131	32446	2.96	3.0E-01	D16313.1	NT	Mouse cyclotactin 15 gene, complete cds
7041	18373	31261	0.71	3.0E-01	U02269.1	NT	Strongyloides purpurus 3467 kDa lamellin-binding protein mRNA, partial cds
7111	20045	33347	0.96	3.0E-01	AF226247.1	NT	Canis lupus familiaris hemagglutinin gene, complete cds
7195	20219	33551	0.59	3.0E-01	X83941.1	NT	S Cerevisiae GAC1
7328	20289	33643	0.82	3.0E-01	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
7549	20512	33870	4.98	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
7744	20695	34064	1.33	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (psaA) gene, partial cds
8259	21228	34638	1.28	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8716	21684		4.13	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clas9), mRNA
8819	21786	35210	1.34	3.0E-01	BE566093.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE3981594 5'
9181	22147	35574	0.74	3.0E-01	AF141078.1	NT	Streptomyces sulfonolactams isopancillin N synthase (pbcC) gene, partial cds
9223	22189		0.71	3.0E-01	7681085	NT	Homo sapiens DRFZP568M0122 protein (DRFZP568M0122), mRNA
9573	22535	35986	0.95	3.0E-01	AF220507.1	NT	Anabaena PCCT120 cytosine-specific DNA methyltransferase (dmrB) gene, complete cds; putative anabaena phosphoribosyltransferase gene, partial cds; and unknown gene
9582	22559	36320	0.51	3.0E-01	P75359	SWISSPROT	HYPOHETICAL 69.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
10327	23251	36730	0.73	3.0E-01	BF574812.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE2283356 5'
10501	23423	36922	0.47	3.0E-01	AF152568.3	NT	Acidobacillus acidofermentans (Tada) (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10501	23423	36922	0.47	3.0E-01	AF152568.3	NT	Acidobacillus acidofermentans (Tada) (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10760	23681	37177	0.95	3.0E-01	AW118111.1	EST_HUMAN	3a03410.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2606036 3'
10762	23683	37179	2.14	3.0E-01	AB030231.1	NT	Aspergillus oryzae btpA gene for ER chaperone BIP, complete cda
10782	23703	37207	0.82	3.0E-01	BF68384.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301097 5'
10782	23703	37207	0.82	3.0E-01	BF68384.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301097 5'
12061	24834	38526	2.5	3.0E-01	H15029.1	EST_HUMAN	y84b10.r1 Soares fetal liver spleen 1NF.S3 Homo sapiens cDNA clone IMAGE:194107 6'
12061	24834	38530	2.5	3.0E-01	H15029.1	EST_HUMAN	y84b10.r1 Soares fetal liver spleen 1NF.S3 Homo sapiens cDNA clone IMAGE:194107 6'
12696	25875		1.57	3.0E-01	AJ267631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12979	25917		2.52	3.0E-01	6677768	NT	Mus musculus ribose 5-phosphate isomerase A (Rplp), mRNA
1747	14778					NT	Mus musculus mas proto-oncogene and lgr2 gene for insulin-like growth factor type 2 and L41ps and A478 pseudogenes
2039	15058	28077	0.92	2.9E-01	AJ246895.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2760	15274	28298	1.2	2.9E-01	AF222718.1	NT	Chrysidodermis synuridensis mitochondrion, complete genome
3265	16319	29240	1.92	2.9E-01	AW754238.1	EST_HUMAN	PM1-CT0326-171289-001-412 CT0326 Homo sapiens cDNA
3265	16319	29241	1.92	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171289-001-412 CT0326 Homo sapiens cDNA
3912	16952	29863	1.03	2.9E-01	AJ610836.1	EST_HUMAN	lp21a11.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gbD16050 NIL-2-A
3955	16995	29911				EST_HUMAN	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
4112	17146		0.81	2.9E-01	AJ769472.1	EST_HUMAN	w14d10.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402803 3' similar to WP-C34F-6.7
4511	17536		0.7	2.9E-01	AW002802.1	EST_HUMAN	CE15676;
4710	17731	30420	1.24	2.9E-01	AA328468.1	EST_HUMAN	4a57612.1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480395 3'
			1.5	2.9E-01	AL163207.2	NT	repetitive element;
5156	18166		1.25	2.9E-01	AJ670896.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
5275	18281	31145	3.3	2.9E-01	AJ130107.1	NT	w60603.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287309 3' similar to contains L1.12 L1
5277	18283	31148	1.12	2.9E-01	BE741380.1	EST_HUMAN	repetitive element;
5330	18436		1.49	2.9E-01	R37485.1	EST_HUMAN	Mus musculus SCI gene locus
5469	20065	33372	0.75	2.9E-01	AF321001.1	NT	001694241F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948178 5'
						NT	Y776712.x1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28281 3'
						NT	Suaeda maritima subsp. salina S-adenosylmethionine synthetase 2 mRNA, complete cds
						NT	B subtilis levansucrase operon lvsC, lvsE, lvsF, lvsG and sacC (partial) genes for fructose phosphotransferase
5558	18948	32133	5.1	2.9E-01	X56098.1	NT	system polypeptides P16,18,28,30, and levansucrase
5558	18948	32134	5.1	2.9E-01	X56098.1	NT	B subtilis levansucrase operon lvsC, lvsE, lvsF, lvsG and sacC (partial) genes for fructose phosphotransferase
5871	18960	32149	6.12	2.9E-01	6878662	NT	system polypeptides P16,18,28,30 and levansucrase
6174	19249	32482	1.35	2.9E-01	AA418145.1	EST_HUMAN	Mus musculus Eph receptor A8 (EphA8), mRNA
						EST_HUMAN	zw67512.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6412	19480	32727	1.05	2.9E-01	AI781128.1	EST_HUMAN	we27c05.x1 NO1_QGAP_Lu24 Homo sapiens cDNA clone IMAGE:23423123 similar to contains L1.H1 L1 repetitive element;
6459	19524	32775	2.3	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6599	19659	32931	0.6	2.9E-01	R09194.1	EST_HUMAN	y93008.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
6599	19659	32932	0.6	2.9E-01	R09194.1	EST_HUMAN	y93008.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
6693	19935		0.84	2.9E-01	Z50156.1	NT	D discoideum gene for 34 kD actin binding protein
7043	20065	33372	0.56	2.9E-01	AF321001.1	NT	Sus scrofa maritima subsp. salsu S-adenosylmethionine synthetase 2 mRNA, complete cds
7179	18410	31211	1.57	2.9E-01	AF142326.1	NT	Mus musculus Filh protein (Filh) gene, complete cds; and Uglh protein (Uglh) gene, partial cds
7303	20274	33610	2.99	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C
7367	20337	33687	1.68	2.9E-01	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fes-binding protein Dxxx (DXXX) gene, partial cds; Bln1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1.3-galactosyl tr>
8262	21221	34630	1.67	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8262	21221	34631	1.87	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8469	21457	34874	0.49	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5a gene, exons 5-19
8469	21457	34875	0.49	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5a gene, exons 5-19
8502	21470		1.16	2.9E-01	BF217743.1	EST_HUMAN	Buchnera aphidicola plasmid pLeu isolate M1 2-isopropylmalate synthase (leuA) gene, partial cds; 3-isopropylmalate dehydrogenase (leuB) gene, complete cds; and isopropylmalate dehydratase subunit (leuC) gene, partial cds
8682	21650		0.45	2.9E-01	AF197456.1	NT	
8842	21908	35333	0.77	2.9E-01	AU150910.1	EST_HUMAN	AU150610 NT24922 Homo sapiens cDNA clone NT2RP2003601 3'
9277	22243	35672	1.01	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonyleurea receptor-like protein mRNA, complete cds
9368	22353	35784	0.6	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9601	22605	36053	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
9601	22605	36054	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
11240	24193	37711	1.7	2.9E-01	AF128543.1	NT	Typanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11497	24440	37689	1.86	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11497	24440	37690	1.86	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11913	24704	36395	2.95	2.9E-01	AI139078.2	NT	Campylobacter jejuni NGCTC11168 complete genome, segment 5/6
12109	24797	36579	2.1	2.9E-01	AW294742.1	EST_HUMAN	U-H-LBWO-aim-4-10-0-J1.61 NCI CGAP Subst Homo sapiens cDNA clone IMAGE:2726994 3'
12651	25334	31780	1.47	2.9E-01	AW005971.1	EST_HUMAN	W26905.x1 NO1_QGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element MER28 repetitive element;
12726	26381	31747	4	2.9E-01	AF092453.1	NT	Homo sapiens TNF-alpha-inducible RNA binding protein (TIRP) gene, complete cds
13025	25573	31694	1.35	2.9E-01	Y08637.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus

Table 4

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13025	25573	31095	1.35	2.0E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
570	13840		2.2	2.8E-01	U87138.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
575	13944		1.41	2.8E-01	L28145.1	NT	Rhino dwarf virus movement protein, complete cds; coat protein, complete cds
1085	14129	27083	3.9	2.8E-01	AF16050.1	NT	Guna guira oocyte maturation factor Mos (c-mos) gene, partial cds
1282	14317	27279	1.08	2.8E-01	BE313442.1	EST_HUMAN	801148733FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163988 5'
1282	14317	27280	1.08	2.8E-01	BE313442.1	EST_HUMAN	801148733FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163988 5'
1285	14330	27291	2.65	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1740	14770	27758	2.22	2.8E-01	AW980020.1	EST_HUMAN	QV1-C10364-120200.065-b05 C10364 Homo sapiens cDNA
2028	15048	28062	2.08	2.8E-01	AL047820.1	EST_HUMAN	DKFZp56812321_j1 588 (synonym: hule1) Homo sapiens cDNA clone DKFZp56812321
2141	15158	28174	1.51	2.8E-01	AW511195.1	EST_HUMAN	hd44003.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2479	15483	28507	2.18	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2479	15483	28508	2.18	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2584	15558		3.07	2.8E-01	AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2874	15971	28689	1.35	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipyltransferase, complete cds
2982	16040		1.48	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat shock protein (HSP90) mRNA, partial cds
2983	16041	28963	2.57	2.8E-01	Z14037.1	NT	B. laurus microsatellite (ETH121)
3390	16439	29566	1.18	2.8E-01	AF000094.1	NT	Prococcus hordoshii O73 genome DNA, 777001-994000 nt, position (477)
4021	17059	29960	1.72	2.8E-01	AE001160.1	NT	Borrelia burgdorferi (section 68 of 70) of the complete genome
4150	17181		0.67	2.8E-01	AE004450.1	NT	Pseudomonas aeruginosa PA01, section 11 of 528 of the complete genome
4228	17265		2.41	2.8E-01	AI090888.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4488	17513	30401	2.62	2.8E-01	P13515	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L-PROTEIN)
4822	17839	30737	0.92	2.8E-01	D19050.1	NT	Human mRNA for transcription factor AREB8, complete cds
4822	17839	30738	0.92	2.8E-01	D19050.1	NT	Human mRNA for transcription factor AREB8, complete cds
4898	17883	30771	2.71	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4897	17914	30804	1.37	2.8E-01	BF528188.1	EST_HUMAN	80204201FT NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180129 5'
4920	17937	30829	1.69	2.8E-01	AI272699.1	EST_HUMAN	q158c11.x1 Soares_NhlMPL_S1 Homo sapiens cDNA clone IMAGE:4180129 5'
5384	25637	31962	23.73	2.8E-01	AA346897.1	EST_HUMAN	repetitive element; contains element LTR5 repetitive element;
5687	18782	31954	2.52	2.8E-01	AB016625.1	NT	EST157072 Infant brain Homo sapiens cDNA 5' end
5915	19001		1.04	2.8E-01	AW932583.1	EST_HUMAN	Homo sapiens OCTN2 gene, complete cds
6028	19111	32313	0.57	2.8E-01	AA785298.1	EST_HUMAN	GM1-BN0024-150200-118-p12 BN0024 Homo sapiens cDNA
							ae01d08.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303681 5' similar to gb:M34539 FK508-BINDING PROTEIN (HUMAN);



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6048	19129		0.49	2.8E-01	AA04576.1	EST_HUMAN	z41101.1 Soares ovary tumor N8HOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element.
6300	25994		0.78	2.8E-01	IM36988.1	NT	Bovine 680 bp repeated unit of 1.728 satellite DNA
6343	19412	32653	2.02	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate adolase mRNA, complete cds
6343	19412	32653	2.02	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate adolase mRNA, complete cds
6895	19947	33244	8.31	2.8E-01	BF511215.1	EST_HUMAN	U1-F-B14-adj-04-04-04.1 s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085192 3'
7201	20225	33557	0.52	2.8E-01	U65300.1	NT	Orthomyxa heterodus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7579	20541	33900	0.51	2.8E-01	BE881455.1	EST_HUMAN	601430157F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3892142 5'
7675	20633		1.03	2.8E-01	U65933.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (bcl) gene, chloroplast gene encoding chloroplast protein, partial cds
7724	20680	34044	0.77	2.8E-01	X63980.1	NT	L.esculentum gp2 mRNA for GTP-binding protein
8429	21398	34808	1.12	2.8E-01	AI346128.1	EST_HUMAN	qp48R01.x1 NCI CGAP C68 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
8429	21398	34809	1.12	2.8E-01	AI346128.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8551	21519	34938	2.25	2.8E-01	U51688.1	NT	qp48R01.x1 NCI CGAP C68 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
8551	21519	34938	2.25	2.8E-01	U51688.1	NT	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8859	21826	35249	0.49	2.8E-01	AA911629.1	EST_HUMAN	Homo sapiens lanastrol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8859	21826	35249	0.49	2.8E-01	AA911629.1	EST_HUMAN	60202905.s1 NCI CGAP C612 Homo sapiens cDNA clone IMAGE:1419993 3' similar to gb:M87789 IG
8936	21902		7.34	2.8E-01	BF347847.1	EST_HUMAN	GAMMA-1 CHAIN C REGION (HUMAN);
8936	21902		7.34	2.8E-01	BF347847.1	EST_HUMAN	60202987F1 NCI CGAP Bn67 Homo sapiens cDNA clone IMAGE:4158525 5'
9821	22670	33127	0.91	2.8E-01	U17251.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds
10069	22986		0.85	2.8E-01	L13654.1	NT	Lyoporelcan esculentum peroxidase (TPX1) mRNA, complete cds
10248	23173	36602	0.93	2.8E-01	AF132728.1	NT	Escherichia coli translocated nitrate receptor Trt (trt) gene, complete cds
10248	23173	36603	0.93	2.8E-01	AF132728.1	NT	Escherichia coli translocated nitrate receptor Trt (trt) gene, complete cds
10310	23242	36716	0.6	2.8E-01	AF294393.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
10420	23342	36828	4.98	2.8E-01	7706163	NT	Homo sapiens hypothetical protein LOC51319, mRNA
10578	23586		0.94	2.8E-01	8528154	NT	Fujinami sarcoma virus, complete genome
10718	23940	37133	0.44	2.8E-01	BE966727.2	EST_HUMAN	601054822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839785 3'
11095	24055	37578	1.9	2.8E-01	BF241062.1	EST_HUMAN	601080794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11095	24055	37579	1.9	2.8E-01	BF241062.1	EST_HUMAN	601080794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11125	24085	37612	2.96	2.8E-01	BF665670.1	EST_HUMAN	601852148F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076028 5'
11008	24346		4.02	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4275853 5'
12312	25120	31843	1.39	2.8E-01	AF298477.1	NT	Ovis aries tissue inhibitor of metalloproteinase 1 (TIMP-1) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12884	26561		23.54	2.8E-01	D83328.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12788	29420	31736	3.09	2.8E-01	BE176699.1	EST_HUMAN	PM4-1170606-030400-001-007 HT0606 Homo sapiens cDNA
12817	25439	31742	1.37	2.8E-01	BE900118.1	EST_HUMAN	601673020F1.NH_MGC_21 Homo sapiens cDNA clone IMAGE:3955996.5'
12969	25979		3.15	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
13097	25973		1.76	2.8E-01	AW026400.1	EST_HUMAN	wu86953.x1 NCL CGAP_K63 Homo sapiens cDNA clone IMAGE:2527928.3
477	13549	26477	2.95	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
615	13890	26566	8.43	2.7E-01	AA450061.1	EST_HUMAN	z639b10.e1 Soares, Intl, feus_N52HF8_5w Homo sapiens cDNA clone IMAGE:789327.3' similar to contains AU repetitive element
12658	14301	27282	2.18	2.7E-01	AB004908.1	NT	Ipomoea purpurea transposable element Tpi100 gene for transposase, complete cds
1625	14658		2.21	2.7E-01	X76815.1	NT	G lamblia SR2 gene
1742	14772	27757	2.88	2.7E-01	W58067.1	EST_HUMAN	2522101.T Soares, Intl, feus_N52HF8_5w Homo sapiens cDNA clone IMAGE:341443.5'
1791	14820	27805	2.49	2.7E-01	PT03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12, CORE PROTEIN P16, CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2145	15985		2.29	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monomine transporter type 2, promoter region and exon 1
2375	15383	28405	6.39	2.7E-01	Y13868.1	NT	Feline Immunodeficiency virus env gene, isolate ITT0088PIU (M86), partial repetitive element
2461	15465	28488	3.97	2.7E-01	AI310858.1	EST_HUMAN	164311.12 NCL CGAP_Luz25 Homo sapiens cDNA clone IMAGE:20468336.3' similar to contains element L1
2909	15968	28891	1	2.7E-01	AF251278.1	NT	Mus musculus serine protease inhibitor 14 (Spl14) mRNA, complete cds
2997	16055		0.91	2.7E-01	BF088294.1	EST_HUMAN	CNH-1170875-080204-385-035 HT0875 Homo sapiens cDNA
4038	17078	28978	1.74	2.7E-01	AB29015.1	EST_HUMAN	wu829111.x1 NCL CGAP_K611 Homo sapiens cDNA clone IMAGE:2462828.3'
4053	17090	28985	0.76	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 8 (ae8) gene, partial cds
4053	17090	28986	0.76	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 8 (ae8) gene, partial cds
4051	17097	28991	2.33	2.7E-01	L77569.1	NT	Homo sapiens DJGeorge syndrome critical region, telomeric end
4828	17546	30837	0.76	2.7E-01	L27516.1	NT	Triticum aestivum (W co66) gene, complete cds
5079	18086		4.11	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-603 CT0286 Homo sapiens cDNA
5339	18444	31187	2.13	2.7E-01	PI17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (CHOX-1.4)
5567	18684		1.11	2.7E-01	AB033171.1	NT	Ascaris suum myriophthalma mitochondrial cytb gene for cytochrome b, partial cds
6478	19541	32787	0.51	2.7E-01	Q00918	SWISSPROT	LATEIN TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN, LARGE SUBUNIT)
6478	19541	32788	0.51	2.7E-01	Q00918	SWISSPROT	LATEIN TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN, LARGE SUBUNIT)
6785	19819	33100	1.06	2.7E-01	AE001094.1	NT	(TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN, LARGE SUBUNIT)

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6765	19819	33101	1.06	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6946	20170	33494	2.1	2.7E-01	Q81554	SWISSPROT	FIBRILLIN 1 PRECURSOR
7253	19988		0.84	2.7E-01	A1540070.1	EST_HUMAN	td081068.x1 NC1 CGAP CLL1 Homo sapiens cDNA clone IMAGE:2075103.3*
7590	20542	33901	0.8	2.7E-01	Q11078	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0663.3 IN CHROMOSOME X
7811	20760	34135	0.86	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7811	20760	34138	0.86	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7952	20853	34285	1.9	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7952	20853	34286	1.9	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8012	20950	34343	0.86	2.7E-01	AA351121.1	EST_HUMAN	EST18740 Infant Brain Homo sapiens cDNA 5' and similar to similar to myosin-binding protein H
8012	20950	34344	0.86	2.7E-01	AA351121.1	EST_HUMAN	EST18740 Infant Brain Homo sapiens cDNA 5' and similar to similar to myosin-binding protein H
8084	21021	34421	0.63	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8196	21166	34576	0.86	2.7E-01	AA013147.1	EST_HUMAN	2635611.x1 Scoville reline N26-4HR Homo sapiens cDNA clone IMAGE:360667.3 similar to contains Alu repetitive element
8300	21329		0.52	2.7E-01	AF046820.1	NT	Citrasius auratus pharyngeal adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8475	21444	34961	0.43	2.7E-01	AF068503.1	EST_HUMAN	MR1-SN0062-100500-002-309 SN0062 Homo sapiens cDNA
8527	21455	34909	0.52	2.7E-01	R39257.1	EST_HUMAN	Y081106.s1 Scoville Infant Brain 1N18 Homo sapiens cDNA clone IMAGE:23511.3*
8634	21602	35025	0.74	2.7E-01	AL161552.2	NT	A. obliquus Indiana DNA chromosome 4, contig fragment No. 52
9112	22078	35505	0.52	2.7E-01	Q14764	SWISSPROT	MAJOR VOLTAGE PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
9392	22347	35779	0.51	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn554
9688	22841	36098	11.09	2.7E-01	Q83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9688	22841	36099	11.09	2.7E-01	Q83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9891	22644		2.17	2.7E-01	P37928	SWISSPROT	FIMBRIN W PROTEIN
10160	23065	36562	0.64	2.7E-01	D89880.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
10411	23363	36593	0.85	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10477	23939	36596	2.83	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATcA) mRNA, complete cds
10611	23533	37029	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10611	23533	37030	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
11163	24121	37648	4.87	2.7E-01	AF070504.1	EST_HUMAN	AV705043 ADR Homo sapiens cDNA clone ADBCOD05.5*
11163	24121	37649	4.87	2.7E-01	AF070504.1	EST_HUMAN	AV705043 ADR Homo sapiens cDNA clone ADBCOD05.5*

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11171	24128	37698	2.31	2.7E-01	AI133269.1	NT	Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12056	24939		2.08	2.7E-01	BE1141035.1	EST_HUMAN	MRO-HIT0087.201059-002 c10 HIT0087 Homo sapiens cDNA
12090	24961		1.52	2.7E-01	Q14181	SWISSPROT	PUTATIVE 60S RIBOSOMAL PROTEIN CAP8.05C
12509	25244	31802	1.39	2.7E-01	AL163261.2	NT	Homo sapiens chromosome 21 segment HS21C081
12757	25758		1.46	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12851	25460		1.83	2.7E-01	Q63627	SWISSPROT	CTD-BINDING SLR-LIKE PROTEIN RA4
12948	25526		3.16	2.7E-01	AF217491.1	NT	Homo sapiens fragile 180 oxidoreductase (FOR) gene, exon 6
470	15541	28470	1.97	2.6E-01	P78411	SWISSPROT	IRQOJIS-CLASS HOMEODOMAIN PROTEIN IRX-2
481	13554		1.5	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1394	14423	27397	1.58	2.6E-01	BE88087.1	EST_HUMAN	601106038F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1431	14465	27441	1.36	2.6E-01	AB013260.1	NT	Glycine max pseudogene for B3 30K
1812	14836	27931	6.4	2.6E-01	AL181472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1912	14936	27932	6.4	2.6E-01	AL181472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
2104	15121		7.48	2.6E-01	AW733132.1	EST_HUMAN	5804d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958461 3' similar to gb:M30072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2480	15484		0.99	2.6E-01	Y12966.1	NT	B. maritimus rbcL gene
2553	15555		8.24	2.6E-01	BE272440.1	EST_HUMAN	601128016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
3108	16165		1.02	2.6E-01	AW974531.1	EST_HUMAN	EST386835 MAGE sequences; MAGM Homo sapiens cDNA
3594	16639	29559	1.02	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA (adenine-N6)methyltransferase (dam) gene, complete cds
3657	16700	29618	2.11	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3982	17022	29932	0.77	2.6E-01	AJ012174.2	NT	Chlamydomonas reinhardtii partial m88 gene for RNase P RNA subunit
3982	17022	29933	0.77	2.6E-01	AJ012174.2	NT	Chlamydomonas reinhardtii partial m88 gene for RNase P RNA subunit
4181	17213	30100	17.99	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-03 BT0630 Homo sapiens cDNA
4384	17412	30298	1.39	2.6E-01	AF175263.1	NT	Enterococcus faecium strain N67-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4522	17547	30434	0.82	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4522	17547	30435	0.82	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4579	17601	30497	1.47	2.6E-01	AA457607.1	EST_HUMAN	aa59607 r1 Stratiotes total RNA 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4877	17698	30656	2.31	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type II chlorophyll a/b-binding protein (Lhcb3*) mRNA, complete cds
4745	17766	30659	1.48	2.6E-01	AF142703.1	NT	Ophrestia radicata maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5007	18021	30909	4.38	2.6E-01	H04958.1	EST_HUMAN	y516a03.t1 Soares placenta N22HP Homo sapiens cDNA clone IMAGE:152288 5'
5081	18091		0.78	2.6E-01	AA884626.1	EST_HUMAN	am33b11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:148805 3'
5414	18517		1.08	2.6E-01	AB035972.1	NT	Paramirium caudatum gene for PAP, complete cds
5524	18623	31558	0.69	2.6E-01	M96060.1	NT	Acetabacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CopAx genes, complete cds
5551	18747		0.71	2.6E-01	AI862398.1	EST_HUMAN	MEK35 repetitive element;
5889	18958	32146	0.68	2.6E-01	AF207550.1	NT	Homo sapiens protein translocase, JM26 protein, UDP-galactose translocase, plm-2 protooncogene homolog plm-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown g*
6189	25993		2.61	2.6E-01	AE001811.1	NT	Thermococcus maritima section 123 of 136 of the complete genome
6325	19395	32637	1.81	2.6E-01	AI582357.1	EST_HUMAN	ts02a12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDLF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 contains element LTR1 repetitive element;
6325	18395	32638	1.81	2.6E-01	AI582357.1	EST_HUMAN	ts02a12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDLF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 contains element LTR1 repetitive element;
6552	19022	32837	1.01	2.6E-01	AI162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 677
6625	19879	33168	0.6	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
6625	19879	33170	0.6	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
7238	20259	33593	0.75	2.6E-01	AB914380.1	EST_HUMAN	w44804.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:M37721 PEPTIDYL-L-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7620	20580	33944	0.72	2.6E-01	BE148961.1	EST_HUMAN	CMPyobacter jejuni NCTC11168 complete genome; segment 416
7663	23698		0.73	2.6E-01	AI139077.2	NT	z952a1.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627672 5'
7700	20658		0.61	2.6E-01	AA196149.1	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome; segment 416
8013	20951	34345	1.53	2.6E-01	R10365.1	EST_HUMAN	y37a03.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:627672 5'
8071	21008	34406	0.65	2.6E-01	Q09855	SWISSPROT	gb:12517.U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8182	21182	34589	1.13	2.6E-01	R02411.1	EST_HUMAN	HYPOPHYSICAL TRP-ASP REPEATS CONTAINING PROTEIN C95E5.01 IN CHROMOSOME I
8235	21205	34610	1.17	2.6E-01	BE144331.1	EST_HUMAN	MRO-HT0186-181186-003-412-HT0186 Homo sapiens cDNA
8480	21449	34866	0.62	2.6E-01	X62941.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8480	21449	34867	0.62	2.6E-01	X62941.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8677	21645	35089	2.87	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCL_CGAP_Bms61 Homo sapiens cDNA clone IMAGE:4150395 5'
8753	21721	35143	1.92	2.6E-01	Q10199	SWISSPROT	HYPOPHYSICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9042	22008	35428	4.08	2.6E-01	BE803039.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9042	22008	35428	4.09	2.6E-01	BE803039.1	EST_HUMAN	RC5-ET10082-310500-021-F10 ET10082 Homo sapiens cDNA
9822	22971	36128	0.89	2.6E-01	X17604.1	NT	S. occidentalis INV. gene for invertase (EC 3.2.1.26)
10098	23022		0.63	2.6E-01	AF057121.1	NT	Lonicera canadensis cytochrome b (cyt b) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10227	23152	36841	1.08	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10227	23162	36842	1.08	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10560	23472		0.61	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10875	23765		0.81	2.6E-01	Y10195.1	NT	Homo sapiens PHEX gene
10876	23898		0.48	2.6E-01	Y15874.2	NT	Danio rerio mRNA for RPTP alpha protein
11864	24736		32.27	2.6E-01	X51755.1	NT	Human lambda-2-immunoglobulin constant region complex (germline)
12288	25091		2.77	2.6E-01	10180655	NT	Mus musculus jerky (Jrk), mRNA
12464	25883		3.3	2.6E-01	BE933491.1	EST_HUMAN	801511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3872812 5'
12528	26257	31905	4.42	2.6E-01	AF318956.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXDY2) gene, complete cds, alternatively spliced
12846	26458		2.01	2.6E-01	D89425.1	NT	Canis coveana mRNA for serine/threonine kinase, complete cds
12974	26539		1.74	2.6E-01	AF141325.2	NT	Homo sapiens histidyl polyphosphatase 1-phosphatase (HPP1) gene, complete cds
13070	26562		3.07	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
241	13340	26285	2.33	2.6E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
242	13340	26285	1.97	2.6E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
255	13352		4.63	2.6E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
833	13880	26844	1.87	2.6E-01	U06084.1	NT	Mus musculus CCR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gpdh-S) gene, complete cds
1123	14167	27119	9.8	2.6E-01	T89837.1	EST_HUMAN	Yel1907.r1 Stragelene Lung (4537210) Homo sapiens cDNA clone IMAGE:117488 5'
1522	14564	27528	1.55	2.6E-01	AL115624.1	NT	Bovine cinerea strain 14 cDNA library under conditions of nitrogen deprivation
1741	14771		5.06	2.6E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4), mRNA
1900	15880	27920	0.84	2.6E-01	BE595604.1	EST_HUMAN	PM4-GT0400-310700-005-008 GT0400 Homo sapiens cDNA
1900	15880	27921	0.94	2.6E-01	BE595604.1	EST_HUMAN	PM4-GT0400-310700-005-008 GT0400 Homo sapiens cDNA
2417	15424		13.88	2.6E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2603	16066		1.09	2.6E-01	AA261987.1	EST_HUMAN	2a11612.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:584682 5'
2644	15941	28065	0.94	2.6E-01	X95310.1	NT	B. taurus mRNA for D-aspartate oxidase
3423	16471		2.83	2.6E-01	AW973471.1	EST_HUMAN	EST1385464 IMAGE resequences, MAGM Homo sapiens cDNA

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3545	16591	29516	0.87	2.5E-01	AF293873.1	NT	Danio rerio papilio YY precursor gene, complete cds
3550	16606	29526	7.94	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3681	16900	29903	1.15	2.5E-01	AF141483.1	EST_HUMAN	w11c07.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780.3
3681	16900	29903	1.15	2.5E-01	AF141483.1	EST_HUMAN	w11c07.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780.3
4098	17100	30223	1.78	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4348	17373		0.99	2.5E-01	Q03314	SWISSPROT	RHB PROTEIN
4780	17600		1.34	2.5E-01	Q27225	SWISSPROT	CHL-2 INHIBITING HORMONE PRECURSOR (Mh)
4780	17600	30658	4.71	2.5E-01	AF007768.1	NT	Chlorostaura fumiferae disjuncta associated protein 2 (DAP2) mRNA, complete cds
4821	17638	30736	2.32	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4840	17657		3.69	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4870	17887	30775	0.64	2.5E-01	BE896785.1	EST_HUMAN	h02311.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3922600.5
5086	18096	30872	0.84	2.5E-01	AW873588.1	EST_HUMAN	WP.YT1F9A_294.D_QE22658.1
5243	18251		0.96	2.5E-01	AA768888.1	EST_HUMAN	replicative element
5399	18502	31380	13.58	2.5E-01	S83390.1	NT	T3 receptor associating cofactor-1 [human, fetal liver, mRNA, 2880 nt]
6070	19151	32383	0.64	2.5E-01	AJ006346.1	NT	Homo sapiens KVLG11 gene
6071	19152		0.87	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6525	19588	32847	0.49	2.5E-01	P22219	SWISSPROT	PROTEIN KINASE YPS15
6780	19835	33118	0.86	2.5E-01	AJ251973.1	NT	Homo sapiens partial fibronectin-1 gene
7245	19980	33277	0.8	2.5E-01	B394138	NT	Rattus norvegicus ribin 3 (RABIN3), mRNA
7575	20537	33806	0.79	2.5E-01	U13992.1	NT	Feline calicivirus CF168 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds, and unknown gene
7604	20585		1.13	2.5E-01	AF134718.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7652	20798	34174	0.68	2.5E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
7696	20841	34223	3.88	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
8177	21147	34556	2.72	2.5E-01	BF109040.1	EST_HUMAN	767a0.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389.3
8188	21158	34557	0.62	2.5E-01	BE880712.1	EST_HUMAN	601653391F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198.3
8588	21536	34936	2.02	2.5E-01	BF036593.1	EST_HUMAN	60145228F2 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809.5
8740	21708	35131	0.67	2.5E-01	P04492	SWISSPROT	EB PROTEIN, SMALL T ANTIGEN (EB19K)
8893	21949	35373	3.37	2.5E-01	H53236.1	EST_HUMAN	y8407.7 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:202501.6
9227	22163	35623	0.81	2.5E-01	M89826.1	NT	Mouse basophil-specific protein (TPX-1) gene, exon 10
9874	22827	36230	16.45	2.5E-01	U86851.2	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit - Database Source	Top Hit Descriptor
9874	22927	36281	16.45	2.9E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP-1 gene, promoter region
9831	22814	36268	2.03	2.9E-01	AF085164.1	NT	Hordium vulgare receptor-like kinase LRK10 gene, partial cds
9931	22814	36269	2.03	2.9E-01	AF085164.1	NT	Hordium vulgare receptor-like kinase LRK10 gene, partial cds
10458	23380	36873	1.7	2.9E-01	AF085164.1	EST_HUMAN	RC3-ST10180-130100-015-a07 ST10180 Homo sapiens cDNA
10707	23628	37124	0.44	2.9E-01	11465652	NT	Porphyra purpurea chloroplast, complete genome
10809	23829	37342	1.58	2.9E-01	AF152248.1	EST_HUMAN	hg40c10.x1 NCL CGAP_U1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element NSR1 repetitive element
10912	23832	37346	1.38	2.9E-01	X69491.1	NT	Musca LINE DNA
10992	23912	37427	0.46	2.9E-01	AF934721.1	EST_HUMAN	wp88611.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468878 3' similar to SW:CEBD_HUMAN P49716 CCAAT/ENHANCER BINDING PROTEIN DELTA
10992	23912	37428	0.46	2.9E-01	AF934721.1	EST_HUMAN	wp88611.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468878 3' similar to SW:CEBD_HUMAN P49716 CCAAT/ENHANCER BINDING PROTEIN DELTA
11413	24357	37892	4.47	2.9E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
12120	24590	38591	2.34	2.9E-01	AF000711.1	NT	Aquifex aeolicus section 43 of 109 of the complete genome
12204	25048	38625	4.55	2.9E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Csa4-4) mRNA, complete cds
12230	25959		5.87	2.9E-01	AF161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
12691	26805	31627	1.64	2.9E-01	AF170072.1	NT	Spodoptera frugiperda CALNUG mRNA, complete cds
555	13825	26543	0.86	2.4E-01	AA938516.1	EST_HUMAN	on7004.s1 Scorea_NFL_T_GB_C_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
848	13905	26864	2.67	2.4E-01	BF376124.1	EST_HUMAN	602132442F1 NIH_MGC_B1 Homo sapiens cDNA clone IMAGE:4271878 5'
1307	14343	27307	15.11	2.4E-01	AJ269680.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1307	14343	27308	15.11	2.4E-01	AJ269680.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1384	14418	27387	1.01	2.4E-01	Y17263.1	NT	Homo sapiens FLI-1 gene, partial
1868	14893		27.14	2.4E-01	AF267753.1	NT	Mammalian crystallin putative potassium channel protein Mkt1p mRNA, complete cds
1918	14940	27936	1.21	2.4E-01	AF257708.1	NT	Zuocys thumidus fructose-1,6-bisphosphatase mRNA, complete cds
2148	15164	28180	0.97	2.4E-01	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2178	15193		1.04	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE RECURSOR (IGA1 PROTEASE)
2271	15284	28310	2.23	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2391	15399	28424	1.66	2.4E-01	BF002171.1	EST_HUMAN	7023404.x1 NCL CGAP_Cot616 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2544	16548	28569	2.37	2.4E-01	Z36534.1	NT	O42946 26S PROTEASE REGULATORY SUBUNIT 6A
2772	15764	28785	2.11	2.4E-01	X71783.1	NT	D. discoideum (Ax3-K) pta gene
2797	15789	28807	3.03	2.4E-01	AF030154.1	NT	S. pombe swi6 gene
						NT	Bovine adenovirus 3 complete genome
3149	16208		3.16	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retroviral (gag/pol) genes, complete cds



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3163	18219	28134	1.71	2.4E-01	X74209.1	NT	H.sapiens AGT gene, Part fragment of intron 4
3676	18718	29632	1	2.4E-01	AF169793.1	NT	Podocarpa anserina HEI-C protein (Hr-C) gene, complete cds
3773	18615	29724	0.95	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4092	17098		0.87	2.4E-01	D28660.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
4074	17889		0.98	2.4E-01	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
5089	18099	30976	0.95	2.4E-01	D00644.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5637	18634	31574	0.77	2.4E-01	AJ925707.1	EST_HUMAN	wd33006.x1 NCI_OGAP_Gas4 Homo sapiens cDNA clone IMAGE:2467129 3'
5637	18634	31676	0.71	2.4E-01	AJ925707.1	EST_HUMAN	wd33006.x1 NCI_OGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5662	18659	31606	0.69	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5738	18632	32011	9.32	2.4E-01	AF091218.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5738	18632	32012	9.32	2.4E-01	AF091218.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5768	18658		0.85	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
5991	25649		1.03	2.4E-01	AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (calM2) gene
5998	18082	32279				EST_HUMAN	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4, contains element TAR1 repetitive element
6098	19177	32395	2.08	2.4E-01	BF692398.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6209	19283	32515	2.02	2.4E-01	AF035546.1	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6264	19337	32570	0.84	2.4E-01	AV733767.1	EST_HUMAN	AV733767 cDNA Homo sapiens cDNA clone cdaADE11 5'
6523	19586	32844	0.69	2.4E-01	AAS98672.1	EST_HUMAN	270402 s1 Soares, testis NHT Homo sapiens cDNA clone IMAGE:727893 3'
6885	19742	33018	1.72	2.4E-01	AJ698989.1	EST_HUMAN	wd62011.x1 NCI_OGAP_Par1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gbJ03464
7247	19952	33276	0.64	2.4E-01	AF163963.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7566	20529	33988	7.03	2.4E-01	L43001.1	NT	Muscle vision tyrosine aminotransferase gene, complete cds
7748	20701	34068	0.55	2.4E-01	N48732.1	EST_HUMAN	Bos taurus guanylate cyclase-activating protein 2 (guac2) mRNA, complete cds
7894	20933		0.51	2.4E-01	U05013.1	NT	Y56511 r1 Soares, multiple sclerosis_2NH-MSP Homo sapiens cDNA clone IMAGE:277460 5'
7996	20935	34328	0.97	2.4E-01	AF229644.1	NT	Rattus norvegicus Sprague-Dawley heme oxygenase-2 non-reducing isoform gene, complete cds
8416	21385	34792	0.51	2.4E-01	X97262.1	NT	Mus musculus DXIm44e protein (DXIm44e) mRNA, complete cds
8416	21385	34793	0.51	2.4E-01	X97262.1	NT	Mus musculus pab gene and promoter
8892	21680	35083	1.5	2.4E-01	AJ012685.1	NT	Mus musculus pab gene and promoter
8946	21912	35337	0.98	2.4E-01	BF242794.1	EST_HUMAN	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
9001	21967		0.57	2.4E-01	BF679275.1	EST_HUMAN	6018776791 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4106289 5'
9437	22451	35891	0.51	2.4E-01	AL139077.2	NT	902086188FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5'
						NT	Campylobacter jejuni NC1011168 complete genome, segment 4/6

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9487	22451	35892	0.51	2.4E-01	AL13077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/8
8921	22742	38193	7.63	2.4E-01	AI693515.1	EST_HUMAN	wtd3402.X1 Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:233080.8 3' similar to contains
10662	22989	38457	0.57	2.4E-01	AF20067.1	NT	MER22.b1 TAR1, repetitive element
10082	22988	38458	0.57	2.4E-01	AF220057.1	NT	Drosophila melanogaster SKPB gene, complete cds
10805	23723	37227	1.89	2.4E-01	Q03992	SWISSPROT	Drosophila melanogaster SKPB gene, complete cds
11189	24079	37603	2.88	2.4E-01	AI161494.2	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11185	24141	37675	1.77	2.4E-01	AF30189.1	NT	Arabis thaliana DNA chromosome 4, contig fragment No. 8
11634	24175		1.52	2.4E-01	Z21847.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
12095	24887	36584	4.86	2.4E-01	P08900	SWISSPROT	P. aculeata model virus genomic RNA
12160	25015	36517	2.5	2.4E-01	AF217491.1	NT	PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR
12284	25748		1.93	2.4E-01	AF004213.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12581	25750		2.1	2.4E-01	AJ278167.1	NT	Arabidopsis thaliana ethylene-insensitive-like1 (EIL1) mRNA, complete cds
12575	25734		2.27	2.4E-01	V01507.1	NT	Mus musculus mRNA for putative mcf7 protein (mcf7 gene)
12782	26945		1.31	2.4E-01	BF228975.1	EST_HUMAN	Gallus gallus gene coding for a-actin
13008	26559		8.48	2.4E-01	AL163261.2	NT	RCS-GT0413-100800-023-006 GT0413 Homo sapiens cDNA
389	13464	26394	0.98	2.3E-01	U75898.1	NT	Homo sapiens chromosome 21 segment HS21C081
638	13704		5.85	2.3E-01	U39713.1	NT	aromatase [Popillia guttata-zabira finches, ovary, mRNA, 3'188 nt]
669	13733	26558	21.34	2.3E-01	U67596.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
934	13987	26937	4.19	2.3E-01	BE311893.1	EST_HUMAN	Methanococcus jannaschii section 138 of 150 of the complete genome
1511	14543	27614	1.33	2.3E-01	6677980	NT	6011420735F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:3505878 5'
							Mus musculus vacuolar protein sorting 4b (Vps4b), mRNA
1688	14601		1.02	2.3E-01	U22837.2	NT	Yersinia pestis HmeH (hmeH), HmsF (hmsF), HmeR (hmsR), and HmsS (hmsS) genes, complete cds
1608	14640	27617	1.21	2.3E-01	AJ246480.1	NT	Brassica napus alg gene for Sucrose glycoprotein, cultivar T2
1638	14688	27644	2.82	2.3E-01	Y10897.2	NT	Mus musculus cdtb gene, exon 1, partial
2081	15079		1.33	2.3E-01	AJ253553.1	EST_HUMAN	Homo sapiens cdtb gene, exon 1, partial
2452	15457	28478	2.76	2.3E-01	BE29718.1	NT	601175592F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3831015 5'
2680	15657	28976	1.27	2.3E-01	M11319.1	NT	Homo sapiens cdtb gene, complete cds
2835	14422	27391	2.34	2.3E-01	AB015033.1	NT	Human erythropoietin gene, complete cds
							Martiniella apocynensis gyrB gene for DNA gyrase subunit B, partial cds, strain:FO 14837
2974	16032	28955	1.25	2.3E-01	AA601376.1	EST_HUMAN	replicative element/contains element THR repetitive element
3100	16157		7.15	2.3E-01	R21732.1	EST_HUMAN	yf21b07.51 Soares placenta N22-IP Homo sapiens cDNA clone IMAGE:130357 3'
3383	16432	28380	1.28	2.3E-01	H08936.1	EST_HUMAN	yf21b10.77 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3894	16994	28796	1.08	2.3E-01	S82821.1	NT	GSTA5-epitubulin S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3996	16996		5.02	2.3E-01	7862133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4212	17241		0.92	2.3E-01	J03287.1	NT	Rat etidil natriuretic factor (ANF) gene, 5' end
4377	17405	30285	0.94	2.3E-01	R62262.1	EST_HUMAN	X1701.1 Source placent N224P Homo sapiens cDNA clone IMAGE:146017 5'
4428	17455		2.24	2.3E-01	L75788.1	NT	Mus musculus retin (Rn-1c) gene, promoter region
4479	17504	30392	1.07	2.3E-01	D90899.1	NT	Mus musculus scin (Rn-1c) gene, promoter region
4515	17540	30426	1.9	2.3E-01	AF092535.1	NT	Synochyale sp. POC6803 complete genome, 1/27, 1-133859
4584	17606	30502	7.42	2.3E-01	5031984	NT	Homo sapiens mitogen-activated protein kinase p3delta (PRKM13) mRNA, complete cds
5087	18097	30973	0.86	2.3E-01	AB032400.1	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5200	18209	31093	0.91	2.3E-01	U01328.1	NT	Mus musculus tulip 1 mRNA, complete cds
5377	18481	31356	2.19	2.3E-01	AB040945.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
5503	18603	31532	2.51	2.3E-01	BF056891.1	EST_HUMAN	Homo sapiens mRNA for KIAA1512 protein, partial cds
5608	18704	31861	4.56	2.3E-01	X96597.1	NT	P03300 GAG POLYPROTEIN CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10J ;
5733	18827		1.01	2.3E-01	L39112.1	NT	C.familialis rom1 gene
5845	18935	32116	0.81	2.3E-01	S60371.1	NT	Vitellogenin coreum small subunit ribosomal RNA gene
6051	19132	32340	2.02	2.3E-01	A708940.1	EST_HUMAN	23S rRNA (Laccosinobacillus caesusus, Genomic, 2866 nt)
6051	19132	32341	2.02	2.3E-01	A708940.1	EST_HUMAN	as27612.xt Barstead acta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6812	19666	33154	0.76	2.3E-01	AF198099.1	NT	as27612.xt Barstead acta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7081	20083	33391	5.28	2.3E-01	A718148.1	EST_HUMAN	as27612.xt Barstead acta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7318	20289	33632	0.89	2.3E-01	9623323	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7505	20470	33830	0.79	2.3E-01	AF000227.1	NT	as27612.xt Barstead acta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7646	20606	33972	2.65	2.3E-01	AF175399.1	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7649	20609	33974	10.72	2.3E-01	A719881.1	EST_HUMAN	Oryctolagus cuniculus cytochrome oxidase subunit Iva (cox1a2) mRNA, complete cds; nuclear gene for mitochondrial product
7649	20609	33975	10.72	2.3E-01	A719881.1	EST_HUMAN	as27612.xt Barstead acta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7866	20810		3.39	2.3E-01	6754779	NT	as27612.xt Barstead acta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7871	20816	34183	1.36	2.3E-01	BE88071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
8028	20955		2.59	2.3E-01	N80093.1	EST_HUMAN	z012a08.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292358 5'
8073	21010	34408	0.63	2.3E-01	11416821	NT	Homo sapiens proboscidea alpha cluster (LOC35860), mRNA
8073	21010	34409	0.63	2.3E-01	11416821	NT	Homo sapiens proboscidea alpha cluster (LOC35860), mRNA
8184	21164	34562	0.8	2.3E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
8326	21295	34710	2.02	2.3E-01	M68931.1	NT	Oryctolagus nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8838	21805	35222	0.54	2.3E-01	U57998.1	NT	Mus musculus preproposit (papp) (SOP-1) gene, complete cds
9125	22091	35519	0.46	2.3E-01	AW390541.1	EST_HUMAN	x58a06.x1 NCI_OGAP_B1938 Homo sapiens cDNA clone IMAGE:2891654 3'
9240	22206	35639	0.45	2.3E-01	AW964460.1	EST_HUMAN	EST1376533 MAGE resequences, MAGE Homo sapiens cDNA
9496	22460	35900	0.69	2.3E-01	AA372164.1	EST_HUMAN	EST184061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63358)
9496	22460	35901	0.69	2.3E-01	AA372164.1	EST_HUMAN	EST184061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63358)
9540	22887	36328	0.63	2.3E-01	6678318	NT	Mus musculus phosphotylinositol 3-kinase catalytic subunit delta (PIK3cd), mRNA
10086	23013	36486	0.78	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2866739 5'
10141	23067	36543	0.69	2.3E-01	AW994480.1	EST_HUMAN	EST1376533 MAGE resequences, MAGE Homo sapiens cDNA
10191	23116	36600	1.36	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
10228	23151	36640	0.57	2.3E-01	AW394633.1	EST_HUMAN	PM2-DT0036-28/289-001-004 DT0038 Homo sapiens cDNA
10284	23219	36702	2.8	2.3E-01	BE173060.1	EST_HUMAN	MRH-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
10351	23275	36749	2.33	2.3E-01	AJ283261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10809	23730	37232	0.8	2.3E-01	AF201629.1	EST_HUMAN	Murine hepatitis virus strain 2, complete genome
10820	23741		6.12	2.3E-01	BF133577.1	EST_HUMAN	601648156R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102082 3'
11355	24305	37832	1.49	2.3E-01	AF004633.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11355	24305	37833	1.49	2.3E-01	AF004633.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11522	24463	38015	1.69	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11622	24463	38016	1.69	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11679	24845	38222	2.61	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome
12088	24959	38556	1.47	2.3E-01	AE004686.1	NT	Pseudomonas aeruginosa PA01, section 229 of 529 of the complete genome
12278	25098		5.42	2.3E-01	U45263.1	NT	Borrelia burgdorferi 29-8 locus, ORF-AD genes, complete cds and REP+ gene, partial cds
12370	25156		6.49	2.3E-01	127231.1	EST_HUMAN	HC0EST144 HT28M8 Homo sapiens cDNA clone HCE44 5'
12403	25178		2.24	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-509 SN0012 Homo sapiens cDNA
12460	25892	31417	2.82	2.3E-01	AW303823.1	EST_HUMAN	x021407.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR-Q82175 Q82175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTRS.b2 TART1 repetitive element ;

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12494	25937	31312	11.07	2.3E-01	BE982464.1	EST_HUMAN	6016072032F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:390869 5'
12544	25267		2.36	2.3E-01	BF683319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4287719 5'
12591	25295		3.71	2.3E-01	AL006519.1	NT	Retus nonvegicus mRNA for acid galacton channel
12680	25348		2.12	2.3E-01	U49645.1	NT	Pleurodeles walli distal-less like protein PDlx-3 (P-Dlx-3) mRNA, complete cds
12926	25511		1.49	2.3E-01	BF475611.1	EST_HUMAN	nc381H12X1 Lupsid scotic nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element nec381 repetitive element;
80	13206	26130	0.89	2.2E-01	AL052190.1	EST_HUMAN	721410.X1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to
1567	14600	27576	2.33	2.2E-01	AF187850.1	NT	Homo sapiens PPAR delta gene, promoter region
2100	15117	28139	2.2	2.2E-01	M34940.1	NT	Fresh-water sponge Em1 alpha collagen (COLF1) gene
2412	15419	28443	8.18	2.2E-01	BF677538.1	EST_HUMAN	602075903F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249669 5'
2593	15594	28611	2.54	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2593	15594	28612	2.54	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2893	15952	28968	4.89	2.2E-01	BE159625.1	EST_HUMAN	PM2-HT0353-281289-033-412 HT0353 Homo sapiens cDNA
2893	15952	28969	4.89	2.2E-01	BE159625.1	EST_HUMAN	PM2-HT0353-281289-033-412 HT0353 Homo sapiens cDNA
2932	15990		1.29	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (PHIT) gene, exon 5
3403	16452		2.28	2.2E-01	AL161582.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 92
3927	16667		0.66	2.2E-01	AF135728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4240	17269		1.2	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4247	17276	30158	5.86	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlik3) and two pore domain K+ channel subunit (Kcnik6) genes, complete cds
4292	17321	30200	2.33	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Meck1) mRNA, complete cds
4292	17321	30201	2.33	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Meck1) mRNA, complete cds
4393	17411	30294	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4393	17411	30295	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4456	17482	30370	23.17	2.2E-01	AW361098.1	EST_HUMAN	RC1-C1070249-141189-021-g04 C1070249 Homo sapiens cDNA
4693	17890		1.38	2.2E-01	D50694.1	NT	Human beta-cytoplasmic actin (ACTB) pseudogene
4698	17895	30773	1.67	2.2E-01	AA211216.1	EST_HUMAN	zsf1c05.1 Stragene RNT neuron (#637233) Homo sapiens cDNA clone IMAGE:645988 5'
5082	18092		1.34	2.2E-01	L13298.1	NT	Mus musculus vinculin gene, exon 3
5160	18169	31048	1.22	2.2E-01	BE141035.1	EST_HUMAN	MRO-HT0067-207099-002-410 HT0067 Homo sapiens cDNA
5181	18190	31066	1.51	2.2E-01	H60548.1	EST_HUMAN	y42109 r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:208001 5' similar to
5263	18271		1.06	2.2E-01	AL163268.2	NT	ph214113.mel1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN); Homo sapiens chromosome 21 segment HS21C066

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5838	18928	32112	2.18	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 158, mRNA
5849	18939		3.59	2.2E-01	D64000.1	NT	Synochocytis sp. POC8803 complete genome, 19/27 2392729-2533899
6114	19192	32415	0.81	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ct-Tbx7) mRNA, complete cds
6114	19192	32416	0.81	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ct-Tbx7) mRNA, complete cds
6854	19917	33211	0.7	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukulin, complete cds
6954	20189	33514	0.58	2.2E-01	AA480108.1	EST_HUMAN	h020606.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839658 3'
6954	20189	33515	0.59	2.2E-01	AA480108.1	EST_HUMAN	h020606.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839658 3'
7222	20244	33578	7.76	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAH009 5'
7336	20307	33650	1.43	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (apA) genes, complete cds; and unknown genes
7336	20307	33651	1.43	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (apA) genes, complete cds; and unknown genes
7509	20474	33834	2.11	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7509	20474	33835	2.11	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7728	20694	34048	0.59	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7966	20905	34297	0.6	2.2E-01	AF287987.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
8000	20939	34332	0.5	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain C-125
8354	21323		2.51	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
8425	21394	34605	1	2.2E-01	Z46933.1	NT	E call sepA and sepB genes
8656	21862	35284	0.49	2.2E-01	AJ132918.1	NT	Pan troglodytes McP2 gene 3'UTR
9234	22200	35629	0.51	2.2E-01	L29312.1	NT	Mouse HD protein mRNA, complete cds
9234	22200	35630	0.51	2.2E-01	L29312.1	NT	Mouse HD protein mRNA, complete cds
9247	22213	35643	4.12	2.2E-01	AE001713.1	NT	Thermotoga maritima section 26 of 136 of the complete genome
9297	22293	35663	0.47	2.2E-01	U09984.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
9376	22441		3.89	2.2E-01	AW85039.1	EST_HUMAN	PH3-CTD253-241239-008-007 CTD253 Homo sapiens cDNA
9470	22434	35872	1.4	2.2E-01	8383247	NT	Mus musculus deformed epidermal autologous factor 1 (Drosophila) (Dcalf), mRNA
9553	22515	35968	1.4	2.2E-01	BF376354.1	EST_HUMAN	MR1-T1N0045-11090-008-002 T1N0045 Homo sapiens cDNA
9644	22588	36037	1.3	2.2E-01	W02988.1	EST_HUMAN	z04069.1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291591 5'
9652	22819	36274	15.89	2.2E-01	P49634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9707	22690	36116	0.69	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (Mkp3)
9718	22748	36197	0.78	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9731	22759	36212	4.39	2.2E-01	M89643.1	NT	Brachydanio rerio spandynin beta and gamma chains (Epd) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9979	22908	36371	0.5	2.2E-01	U90980	SWISSPROT	CYCLOC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10174	23099	36579	3.74	2.2E-01	AF167841.1	NT	Funaria hygrometrica chloroplast localized small heat shock protein (CPaHSP21) mRNA, complete cds;
10313	23237	36719	1.76	2.2E-01	BF206507.1	EST_HUMAN	nuclear gene for chloroplast product
10337	23459	36956	1	2.2E-01	9625671	NT	Human herpesvirus 5, complete genome
10697	23619	37113	0.52	2.2E-01	T59472.1	EST_HUMAN	X653408.f1 Stratiagene ovary (X637217) Homo sapiens cDNA clone IMAGE:75855 5'
10697	23619	37114	0.52	2.2E-01	T59472.1	EST_HUMAN	X653408.f1 Stratiagene ovary (X637217) Homo sapiens cDNA clone IMAGE:75855 5'
10735	23557	37150	0.51	2.2E-01	AF088264.1	NT	Pseudomonas aeruginosa quinoxaline ethanol dehydrogenase (oxaA) gene, partial cds; cytochrome c550 precursor (oxaB), NAD+ dependent acetaldehyde dehydrogenase (oxaC), and pyrodoquinone sulfone synthesis A (pqoA) genes, complete cds, and pyrodoquin-
10810	23731	37274	0.68	2.2E-01	AF071001.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10858	23776	37275	0.67	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11751	24636	38215	3.77	2.2E-01	X01918.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11789	23944	37466	3.41	2.2E-01	7708215	NT	Drosophila 68C glx gene cluster
12317	25860		2.32	2.2E-01	U92671.2	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
12406	25179		3.88	2.2E-01	AF188943.1	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), callicrein (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and U>
12513	17482	30370	6.62	2.2E-01	AW361098.1	EST_HUMAN	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12514	25246		1.7	2.2E-01	AW661922.1	EST_HUMAN	RC1-CT0246-141199-021-g04 CT0249 Homo sapiens cDNA
13111	25948		1.36	2.2E-01	AF271265.1	EST_HUMAN	PTDpous singurus uncoupling protein 3 mRNA, partial cds
972	14024	26978	1.58	2.1E-01	AA565289.1	EST_HUMAN	mi3161.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1081804
975	14026	26980	1.06	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1128	14169		2.38	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1203	14242	27169	0.98	2.1E-01	6754269	NT	Mus musculus interferon (alpha and beta) receptor 2 (Inar2), mRNA
1203	14242	27200	0.98	2.1E-01	6754269	NT	Mus musculus interferon (alpha and beta) receptor 2 (Inar2), mRNA
1512	14544	27515	1.05	2.1E-01	AL249896.1	NT	Mus musculus mas proto-oncogene and Igf2 gene for insulin-like growth factor type 2 and L41ps and A176 pseudogenes
1929	14953	27949	1.94	2.1E-01	AA90824.1	EST_HUMAN	ak73602.at NCI_CGAP_G44 Homo sapiens cDNA clone IMAGE:1919610 3' similar to gb.k02785
2165	15161	28201	3.26	2.1E-01	BF665073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2489	15895	28516	2.19	2.1E-01	HT3908.1	EST_HUMAN	602083.128F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4247503 5'
							yu0407.at Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:232637 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2489	15895	28517	2.19	2.1E-01	H73968.1	EST_HUMAN	WU4047.31 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:232837.3
2636	15994	28914	2	2.1E-01	6812445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (seg-related) member 4 (KCNH4), mRNA
3481	16507	28428	0.92	2.1E-01	AA639482.1	EST_HUMAN	ng00610.st NCI_CGAP_C68 Homo sapiens cDNA clone IMAGE:1159579.3
3819	16859		6.5	2.1E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
4045	17083		1.18	2.1E-01	AE001793.1	NT	Thermococcus maritima section 105 of 138 of the complete genome
4084	17118	30013	1.48	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4084	17118	30014	1.48	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4403	17431		1.62	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4607	17628	30520	1.75	2.1E-01	AB010273.1	NT	Homo sapiens pihap-17 gene, complete cds
5093	18073	30983	5.08	2.1E-01	D13567.1	NT	Lampbrush RNA for alpha-2-macroglobulin, complete cds
5110	18120	30994	1.13	2.1E-01	Q01338	SWISSPROT	ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)
5216	18225	31059	0.92	2.1E-01	AE001526.1	NT	Helicobacter pylori, strain J99 section 87 of 132 of the complete genome
5374	18479	31362	5.48	2.1E-01	BF672686.1	EST_HUMAN	Helicobacter pylori, strain J99 section 87 of 132 of the complete genome
7071	20093	33403	1.16	2.1E-01	AJ22392.1	NT	Drosophila melanogaster 16S rRNA gene, partial
7083	20017	33320	1.92	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7839	20596	33959	0.78	2.1E-01	Q01959	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7839	20596	33960	0.78	2.1E-01	Q01959	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7848	20608		2.34	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7873	20912	34303	1.77	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT18) gene, complete cds
8027	20964	34359	1.08	2.1E-01	AF068887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8027	20964	34360	1.08	2.1E-01	AF068887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8086	21022		0.51	2.1E-01	T87364.1	EST_HUMAN	y885b01.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:114783.5
8407	21376		1.04	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.13), mRNA
8647	21814	35234	5.05	2.1E-01	U68369.1	NT	Haemophilus influenzae hmd, putative haemoglobin processing protein (hmcC), putative ABC transporter (hmcB), putative haemoglobin structural protein (hmcA), and haemoglobin immunity protein (hmcI) genes, complete cds
9149	22115	35540	0.84	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814.1_1331 (synonym: hsc3) Homo sapiens cDNA clone DKFZp434H0814.5
9149	22115	35541	0.84	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814.1_1331 (synonym: hsc3) Homo sapiens cDNA clone DKFZp434H0814.5
6992	22357	35787	6.08	2.1E-01	Z35786.1	NT	S. cerevisiae chromosome II reading frame ORF YBL025w
9862	22768	36251	0.59	2.1E-01	N42558.1	EST_HUMAN	y711et0.11 Soares melanocyte 2N2HM Homo sapiens cDNA clone IMAGE:270954.5
9862	22768	36252	0.59	2.1E-01	N42558.1	EST_HUMAN	y711et0.11 Soares melanocyte 2N2HM Homo sapiens cDNA clone IMAGE:270954.5



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9871	22824	38277	2.77	2.1E-01	X97378.1	NT	A.thaliana mRNA for ARABBP1b protein
9876	22903	38387	1.28	2.1E-01	AB006529.1	NT	Homo sapiens p33r2 gene for ribonucleotide reductase, exon 6
10692	23614	37109	1.13	2.1E-01	Z97087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10725	23647	37140	2.89	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10731	23653	37146	0.93	2.1E-01	BF574254.1	EST_HUMAN	(80 KD) DIACYLGLYCEROL KINASE
11009	23974	37498	3.09	2.1E-01	AF294296.1	NT	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'
11890	24771		2.15	2.1E-01	11036647	NT	Anolis lineatus isolate NG NADH dehydrogenase subunit 2 (ND2) gene, complete cds, mitochondrial gene for mitochondrial product
11905	24786	38376	1.61	2.1E-01	BE180422.1	EST_HUMAN	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
12137	25002		1.38	2.1E-01	X57624.1	NT	RC3-H1T0622-040500-013-b11 HT0622 Homo sapiens cDNA
12660	25339		1.94	2.1E-01	AF217490.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12890	25860		1.8	2.1E-01	L32588.1	NT	Homo sapiens fragile 160 octo reductase (FOR) gene, exons 8, 9, and partial cds
12914	25463		2	2.1E-01	BE622149.1	EST_HUMAN	Human granulosa gene
13045	25886	31682	1.62	2.1E-01	BE672330.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE3915675 5'
201	13302	26231	1.32	2.0E-01	AB017437.1	NT	7a59a02.x1 NCJ CGAP GC68 Homo sapiens cDNA clone IMAGE3228034 3'
535	13966		1.82	2.0E-01	7705801	NT	Gallus gallus mRNA for avian, complete cds
700	13762	26694	1.25	2.0E-01	M177085.1	NT	Homo sapiens CGH-18 protein (LOC51008), mRNA
811	13969	26818	1.56	2.0E-01	AF027865.1	NT	O.cuniculus germline IgH heavy chain V-H1 pseudogene, allele type VHe2
1013	14061	27012	0.72	2.0E-01	D90005.1	NT	Mus musculus Major Histocompatibility Locus class II region
1127	14170	27121	2.83	2.0E-01	AL163213.2	NT	Synechocystis sp. PCC6803 complete genome, 7127_781449-920915
1259	14294	27258	1.42	2.0E-01	AJ132955.5	NT	Homo sapiens chromosome 21 segment HS21C013
1311	14347	27313	2.04	2.0E-01	AW384637.1	EST_HUMAN	Homo sapiens rac1 gene
1454	14487		1.39	2.0E-01	AJ243957.1	NT	PM1-HT0422-281299-002-c08 HT0422 Homo sapiens cDNA
1483	14516	27490	15.27	2.0E-01	4503408	NT	Plum pox virus strain M, complete genome, isolate PS
1555	14587	27569	2.13	2.0E-01	AB007974.1	NT	Homo sapiens dyadbrexin, alpha (DTNA), mRNA
1890	14592		1.52	2.0E-01	AF260700.1	NT	Homo sapiens mitochondrion 1 specific transcript KIA00505
1706	14735	27718	1.38	2.0E-01	U22346.1	NT	Homo sapiens sodiumiodide symporter mRNA, partial cds
1730	14760		2.09	2.0E-01	AF111170.3	NT	Human tryptophan B1 receptor (brady1) gene, complete cds
1772	14801		3.8	2.0E-01	U67525.1	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1907	14831	27928	0.94	2.0E-01	BE871330.1	EST_HUMAN	Methanococcus jannaschii section 87 of 150 of the complete genome
1907	14831	27927	0.84	2.0E-01	BE871330.1	EST_HUMAN	60144941F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3853330 5'
2355	15364		1.88	2.0E-01	X92877.1	NT	60144941F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3853330 5'
							H. sapiens Na+-D-glucose cotransport regulator gene

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3499	16546	29472	0.74	2.0E-01	P46907	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3592	16627		0.82	2.0E-01	AW238005.1	EST_HUMAN	XP15002.X1 NC1_CGAP_JH99 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 repetitive element
3720	16763	29574	0.79	2.0E-01	P34641	SWISSPROT	CEP-11 PROTEIN
3855	16805	29799	1.14	2.0E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3977	17017	29931	0.7	2.0E-01	Z46905.1	NT	Sus scrofa
4597	17618		10.26	2.0E-01	BE826165.1	EST_HUMAN	QY4-EN0032-190600-223-ec3 EN0032 Homo sapiens cDNA
5078	18088	30968	7.06	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5144	18153	31033	0.97	2.0E-01	Y19216.1	NT	Homo sapiens putative palh1bD pseudogene for hair keratin, exons 1 to 9
5298	18302	31163	0.83	2.0E-01	BE439491.1	EST_HUMAN	HTM1-122F1 HTM1 Homo sapiens cDNA
5520	18619	31653	2.31	2.0E-01	X36600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5631	18921	32104	1.89	2.0E-01	X61856.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5640	19026	32220	0.69	2.0E-01	X61856.1	NT	F. rubripes DNA encoding for vav1-RNA synthetase
6178	19253	32489	5.47	2.0E-01	U15300.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6298	19370		0.79	2.0E-01	M75957.1	NT	Human hepatocyte growth factor gene, exon 1
9417	19484	32733	0.96	2.0E-01	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9569	19629	32895	3.06	2.0E-01	X61033.1	NT	M. auratus mu class glutathione transferase gene
9679	19736	33012	4.25	2.0E-01	AW360965.1	EST_HUMAN	PM1-CT0247-141059-001-g06 CT0247 Homo sapiens cDNA
7512	20471	33839	1.27	2.0E-01	AF250371.1	NT	Mus musculus phosphonucleotidase-1 C isozyme (Pfic) gene, exons 3 through 7
7679	20637	33999	0.72	2.0E-01	P54422	SWISSPROT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
8054	20691	34089	0.61	2.0E-01	V00726.1	NT	Mouse germ line gene coding for beta-globin (gamma)
8285	21254		6.17	2.0E-01	AF028026.1	NT	Andes Virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
8542	21510	34927	3.1	2.0E-01	X61151.1	NT	M. musculus scp2 gene exon 14
9074	22049		0.43	2.0E-01	BE562247.1	EST_HUMAN	601344646F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677794.6
9706	22689	36115	1.09	2.0E-01	U92511.1	NT	Dicystatium discidium random slug cDNA19 protein (act19) mRNA, partial cds
9745	22698	36141	0.76	2.0E-01	U71122.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
10103	23029	36506	0.62	2.0E-01	AE001278.1	SWISSPROT	Chlamydia trachomatis section 5 of 67 of the complete genome
10103	23028	36507	0.62	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
10281	23176		1.94	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
10401	23323	36807	1.94	2.0E-01	AF146892.1	NT	Homo sapiens fibronin 2 (FN2) mRNA, complete cds
10401	23323	36808	1.94	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10528	23430	36948	0.84	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10528	23450	36949	0.64	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10575	23497		0.78	2.0E-01	X78388.1	NT	D.melanogaster DNA mobile element (hoppla)
10770	23691	37188	0.97	2.0E-01	XG7121.1	NT	R.norvegicus mRNA for NTR2 receptor
11189	24145	37678	2.24	2.0E-01	D86088.1	NT	Salvelinus plusivus mRNA for transferrin, complete cds
11189	24145	37679	2.24	2.0E-01	D86088.1	NT	Salvelinus plusivus mRNA for transferrin, complete cds
12841	25325		1.42	2.0E-01	AF206837.2	NT	Plimothales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12828	25779		1.86	2.0E-01	AF302773.1	NT	Homo sapiens nitric-oxide synthase (NOS3) mRNA, complete cds
12837	25711	31809	1.34	2.0E-01	AW975297.1	EST_HUMAN	EST387403 MAGIE resequences, MAGN Homo sapiens cDNA
12875	25508	31707	4.12	2.0E-01	A023592.1	EST_HUMAN	ov60a10.5' Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1643810 3'
12898	25483		2.98	2.0E-01	A078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
110	13221		8.6	1.9E-01	7549743	NT	Rattus norvegicus A77 hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
352	13441	26386	8.09	1.9E-01	A004333.1	NT	Mus musculus pale ear (gp) gene, wild type allele, 3' region, partial cds
657	13723	26647	2.86	1.9E-01	U02581.2	NT	Homo sapiens lambricola protein kinase C-interacting protein mRNA, complete cds
657	13723	26648	2.86	1.9E-01	U02581.2	NT	Homo sapiens lambricola protein kinase C-interacting protein mRNA, complete cds
664	13730	26655	8.99	1.9E-01	BE070801.1	EST_HUMAN	RC3-B10502-251199-011-401 BT0502 Homo sapiens cDNA
665	13730	26655	8.99	1.9E-01	BE070801.1	EST_HUMAN	RC3-B10502-251199-011-401 BT0502 Homo sapiens cDNA
888	14039		1.19	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (IL2rg), mRNA
1108	14150	27101	9.83	1.9E-01	AA358813.1	EST_HUMAN	EST167784 Fetal lung II Homo sapiens cDNA 5' end
1372	14409	27376	2.8	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1430	14464		3.22	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (cbp-2) gene, complete cds
2390	15398	28423	3.89	1.9E-01	U86068.1	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2934	15892	28812	3.47	1.9E-01	U86068.1	NT	Sigmund hispidus p53 gene, partial cds
2949	16006		4.89	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3408	16455	29378	4.89	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3482	16539	29484	5.96	1.9E-01	R16467.1	EST_HUMAN	Y14210.1 Scores fetal liver spleen (NLS) Homo sapiens cDNA clone IMAGE:126547 5'
3817	16857	29763	0.87	1.9E-01	AF284017.1	NT	Rattus norvegicus arylamidase deacetylase gene, complete cds
3843	16888	29791	2.26	1.9E-01	P39788	SW/ISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
4018	17057	29599	3.91	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4110	17144	30038	1.42	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271169-045-b11 CT0315 Homo sapiens cDNA
4259	17288	30160	1.24	1.9E-01	BE634943.1	EST_HUMAN	MRI-FN0010-280700-007-404 FN0010 Homo sapiens cDNA
4466	17521	30408	0.83	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 5
5047	18060		1.15	1.9E-01	AF223942.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5231	18239		1.01	1.9E-01	A0831198.1	EST_HUMAN	PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5685	18780		5.2	1.9E-01	AW130146.1	EST_HUMAN	x128a07.x1 NCI_QGAP_UH1 Homo sapiens cDNA clone IMAGE:2618444 3' similar to gb:M73779 RETINOID ACID RECEPTOR ALPHA-1 (HUMAN);
5729	18822	32002	8.11	1.9E-01	AF127937.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5839	18025	32219	0.71	1.9E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5887	15072		2.16	1.9E-01	AU153116.1	EST_HUMAN	AU153116 NT28P4 Homo sapiens cDNA clone IMAGE:2384089 3'
6461	19526	32776	0.95	1.9E-01	AU1762391.1	EST_HUMAN	wf54022.x1 NCI_QGAP_Cot18 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X09559 ATP
6527	16950	32850	0.88	1.9E-01	AW146452.1	EST_HUMAN	SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7164	18395	31240	1.46	1.9E-01	AF43212.1	EST_HUMAN	y05a07.2.s1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MERT3 repetitive element 1;
7193	20217	33547	0.95	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7193	20217	33548	0.95	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7474	20440	33798	0.65	1.9E-01	U73946.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7709	20686	34093	0.75	1.9E-01	U93088.1	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tsst), enterotoxin (ent), and integrase (int) genes, complete cds
7734	20689	34093	1.35	1.9E-01	U90922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPPB) gene, complete cds
7784	20737	34109	2.54	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
8318	21287	34701	1.41	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
9034	22000	35421	12.88	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
9297	22263	35692	1.32	1.9E-01	MF4568.1	NT	Marasipal cat beta-globin gene mRNA, partial cds
9297	22263	35693	1.32	1.9E-01	MF4568.1	NT	Marasipal cat beta-globin gene mRNA, partial cds
10234	23159	36847	0.67	1.9E-01	AA912486.1	EST_HUMAN	dbg010.s1 NCI_QGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element
10802	23524	37019	0.72	1.9E-01	BE630353.1	EST_HUMAN	RCSE-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10802	23524	37020	0.72	1.9E-01	BE630353.1	EST_HUMAN	RCSE-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
11106	24066	37588	1.87	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11831	24714	38298	1.47	1.9E-01	M22263.1	NT	Rattus norvegicus sodium channel 1 mRNA, complete cds
12033	24909	38504	3.54	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12049	24822	38519	1.53	1.9E-01	AJ7344.1	NT	Influenza A/Guangdong/043772 nucleoprotein (seg 5) gene, 5' end
12975	25540		1.82	1.9E-01	AF036959.1	NT	Rattus norvegicus nuclear serine/threonine protein kinase mRNA, complete cds
34	13154	28055	2.78	1.9E-01	U73200.1	NT	Mus musculus p116Rjp mRNA, complete cds
260	15837	28281	1.39	1.8E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
370	13466	26386	1.91	1.8E-01	4502532	NT	Homo sapiens cadmium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
983	14034	26986	0.89	1.8E-01	AI912212.1	EST_HUMAN	wf1102.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1093	14138	27087	1.05	1.8E-01	AF000580.1	NT	Dicystidium discidium plasmid Ddp5, complete genome
1293	14328	27290	9.43	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1503	14536	27507	1.17	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1503	14536	27508	1.17	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1864	14889		1.37	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1882	14907		1.47	1.8E-01	AI733706.1	EST_HUMAN	gp22a10.x6 NC1_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:075936 075936
1930	14954	27950	1.66	1.8E-01	AB051897.1	NT	GAMMA BUTYROBETAINE HYDROXYLASE ;
2702	15998		3.94	1.8E-01	AB051897.1	EST_HUMAN	Mus musculus Scya9, Scya9, Scya9, Scya9 genes for small inducible cytokine A8 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2908	15987		1.95	1.8E-01	AF184589.1	NT	QV3-DT0018-081256-036-g04 DT0018 Homo sapiens cDNA
2914	15972	28896	0.85	1.8E-01	AW182300.1	EST_HUMAN	Junospidulum scutula LEAFY protein (LEAFY2) gene, partial cds
3141	16199	29108	1.35	1.8E-01	AW965176.1	EST_HUMAN	X47a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3379	16428	29354	0.32	1.8E-01	BF183582.1	EST_HUMAN	QV0-HN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3637	16680	29594	1.69	1.8E-01	H03399.1	EST_HUMAN	601809723RT NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4046621 3'
3637	16680	29595	1.69	1.8E-01	H03399.1	EST_HUMAN	Y45601.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
4360	17387		0.75	1.8E-01	D37954.1	NT	Y45601.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
4596	17608	30603	6.42	1.8E-01	AL161556.2	NT	repetitive element;
							Bovine NB26 mRNA for MHC class II (BoLA-DQB), complete cds
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4806	17623	30718	2.5	1.8E-01	AB051897.1	NT	Mus musculus Scya9, Scya9, Scya9, Scya9 genes for small inducible cytokine A8 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5051	18063	30941	2.11	1.8E-01	X79794.1	NT	N. laibacum mRNA pHLA-35
5084	18094	30970	1.98	1.8E-01	AW1814270.1	EST_HUMAN	MF3-ST0203-151269-112-g08 ST0203 Homo sapiens cDNA
5099	18109	30982	0.93	1.8E-01	AF782882.1	EST_HUMAN	an2807.x5 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5131	18140	31018	2.96	1.8E-01	AF181266.1	NT	Mesorhynchus auratus Ne-tauricholate cotransporting polypeptide mRNA, partial cds
5214	18223		0.73	1.8E-01	U66190.1	NT	Coligo forbesi TTA repeat microsatellite region 1.6r-4
5371	18476	31349	0.64	1.8E-01	BE082626.1	EST_HUMAN	RC6-BT0841-300300-011-H03 BT0841 Homo sapiens cDNA
5906	18992	32163	1.91	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12301	28112	31840	1.88	1.8E-01	BF346923.1	EST_HUMAN	602189228F1 NC1 CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155318 5'
12782	29398		2.05	1.8E-01	Q96882	SWISSPROT	DNA TERMINAL PROTEIN (BELT-TT PROTEIN) (PTP PROTEIN)
12866	29488		1.85	1.8E-01	R24494.1	EST_HUMAN	YH4810.1 Scores placenta N22MP Homo sapiens cDNA clone IMAGE:133027 5'
12907	29488		1.56	1.8E-01	Y11114.1	NT	Edipar mRNA for hexokinase (hkt1)
579	13648	26361	1.77	1.7E-01	BE385104.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815768 5'
808	13648	26814	2.22	1.7E-01	Q53330.1	NT	P dimethyl histone gene cluster for core histones H2A, H2B, H3 and H4
982	14015		1.83	1.7E-01	P36616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1868	15019		3.18	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2871	15931	28948	2.3	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpb) gene, partial cds, hemagglutinin/protease regulatory protein (harpR) gene, complete cds, and YRAL VIBCO gene, partial cds
2871	15931	28949	2.3	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpb) gene, partial cds, hemagglutinin/protease regulatory protein (harpR) gene, complete cds, and YRAL VIBCO gene, partial cds
2838	15995	28917	1.88	1.7E-01	AA336909.1	EST_HUMAN	EST41681 Endometrial tumor Homo sapiens cDNA 5' and
3010	16068	28888	1.22	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3010	16068	28889	1.22	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3122	16179	29089	1.88	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3378	16427	29353	0.82	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambica ZAP Express Homo sapiens cDNA clone J2346 5'
3462	16508	29426	1.48	1.7E-01	AJ268505.1	NT	Anabaena sp. ORF4 (partial), ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3598	16998	29814	5.89	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment, partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/TEL gene
4591	17912		1.9	1.7E-01	X52836.1	NT	Schistosoma gregaria alpha repetitive DNA
4878	17893	30782	1.21	1.7E-01	AJ247835.1	EST_HUMAN	qh57e03.x1 Soares_fetal_liver_spleen_1NFLS_31 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF b1 ORF repetitive element:
5165	18174		0.92	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme IIs (ae) gene, complete cds
5210	18219	31095	0.74	1.7E-01	BF030010.1	EST_HUMAN	601557256F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
5482	18582	31493	1.88	1.7E-01	AA470868.1	EST_HUMAN	nt15a02.61 NC1 CGAP_Co3 Homo sapiens cDNA clone IMAGE:881068 3' similar to gb:M17888 60S
5482	18582	31494	1.88	1.7E-01	AA470868.1	EST_HUMAN	nt15a02.61 NC1 CGAP_Co3 Homo sapiens cDNA clone IMAGE:881068 3' similar to gb:M17888 60S
5674	18769	31941	0.74	1.7E-01	U43599.1	NT	ADIC RIBOSOMAL PROTEIN P1 (HUMAN);
6463	19528	32777	12.89	1.7E-01	HT2118.1	EST_HUMAN	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
							Y202908.61 Soares fetal liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:213558 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6526	19589	32848	0.9	1.7E-01	AJ370976.1	EST_HUMAN	ta29c11.x1 Scores, fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6526	19589	32849	0.9	1.7E-01	AJ370976.1	EST_HUMAN	ta29c11.x1 Scores, fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
7031	18363	31250	0.78	1.7E-01	BE300286.1	EST_HUMAN	60094-4067T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2600248 3'
7053	20085		1.78	1.7E-01	AF026532.3	NT	Mesocricetus auratus orviductin precursor (OV) gene, complete cds
7196	20220		0.78	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7430	20397	33749	1.56	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7515	20480	33841	8.55	1.7E-01	BE734179.1	EST_HUMAN	60156022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843564 5'
7721	20078	34043	1.42	1.7E-01	P16724	SWISSPROT	PROBABLY PROCESSING AND TRANSPORT PROTEIN UL56 (HLEF0 PROTEIN)
7739	26688	34057	0.71	1.7E-01	Q01985	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
8194	21104	34573	1.24	1.7E-01	AF000573.1	NT	Homo sapiens homotransferrin 1,2-dioxygenase gene, complete cds
8295	21265	34676	0.62	1.7E-01	AF150699.1	NT	Pseudomonas putilla long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8620	21588	35004	7.37	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3) mRNA
9045	22011	35433	0.6	1.7E-01	AW692873.1	EST_HUMAN	RC2-BN0032-120200-071-a10 BN0032 Homo sapiens cDNA
9196	22162	35468	3.22	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
9196	22162	35591	0.81	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9439	22314	35739	0.44	1.7E-01	R77002.1	EST_HUMAN	X66902.1 Scores placenta N22P Homo sapiens cDNA clone IMAGE:144242 5'
9523	22486	35983	0.43	1.7E-01	BE263142.1	EST_HUMAN	60116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9523	22496	35934	0.43	1.7E-01	BE263142.1	EST_HUMAN	60116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9948	22875	36337	8.16	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
10056	22883	36451		1.7E-01	AW677455.1	EST_HUMAN	EST389564 MAGE resequences, MAGE Homo sapiens cDNA
10056	22883	36462	0.47	1.7E-01	AW677455.1	EST_HUMAN	EST389564 MAGE resequences, MAGE Homo sapiens cDNA
10073	23000	36470	1.93	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
10148	23074	36548	0.59	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (87.05) env gene (partial)
10148	23074	36549	0.59	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (87.05) env gene (partial)
10167	23082	36570	0.7	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6) (sp5 gene)
10653	23515		2.43	1.7E-01	AL163264.2	NT	Homo sapiens chromosome 21 segment HS21C084
10759	23680	37176	1.24	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA
10761	23682	37178	1.81	1.7E-01	AA627872.1	EST_HUMAN	nc60607.st NCI CGAP Co6 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gbL25081
10963	23886		0.42	1.7E-01	AL161542.2	NT	TRANSFORMING PROTEIN RHOC (HUMAN)
11040	24004	37530	8.17	1.7E-01	BE390835.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11167	24116	37641	2.51	1.7E-01	AA814617.1	EST_HUMAN	cd3a03.s1 NCI_CGAP_CNST Homo sapiens cDNA clone IMAGE:1426924 3'
11447	24390	37633	8.03	1.7E-01	7106300	NT	Mus musculus adenomatous polyposis coli binding protein Eb1 (Eb1), mRNA
11447	24390	37634	8.03	1.7E-01	7106300	NT	Mus musculus adenomatous polyposis coli binding protein Eb1 (Eb1), mRNA
11703	24668	38245	1.6	1.7E-01	AA863375.1	EST_HUMAN	af4509.s1 Soares_NFL_I_5BC_S1 Homo sapiens cDNA clone IMAGE:1460267 3'
12021	24898		1.66	1.7E-01	P15272	SWISSPROT	HAIP NUCLEOSIDASE
12141	25005	38815	1.74	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
12273	25893		1.54	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12437	26726	31618	1.55	1.7E-01	AA847421.1	EST_HUMAN	cd1802.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1386291
12555	26726		1.69	1.7E-01	AA847421.1	EST_HUMAN	cd1802.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1386291
12555	26726		1.69	1.7E-01	AA847421.1	EST_HUMAN	cd1802.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1386291
12583	25450	31723	14.15	1.7E-01	U01317.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN)
126	13233	25162	2.02	1.6E-01	AF217532.1	NT	Human beta globin region on chromosome 11
580	15814	26670	1.56	1.6E-01	R31497.1	EST_HUMAN	Homo sapiens mevalonate kinase gene, exon 6 and 7
1304	14537	27509	1.4	1.6E-01	AA546866.1	EST_HUMAN	h23412.s1 NCI_CGAP_Cc11 Homo sapiens cDNA clone IMAGE:135569 5'
1525	14557	27528	4.54	1.6E-01	AF298117.1	NT	h23412.s1 NCI_CGAP_Cc11 Homo sapiens cDNA clone IMAGE:1014639 3'
1941	14865	27602	1.79	1.6E-01	P22068	SWISSPROT	Homo sapiens homeobox protein OTX2 gene, complete cds
2001	15023		1	1.6E-01	U10334.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2393	15892	28427	0.89	1.6E-01	X94232.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2501	15904	28531	1.19	1.6E-01	AB037726.1	NT	H. sapiens mRNA for novel T-cell activation protein
2502	15961	28881	10.42	1.6E-01	AF165860.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2502	15961	28882	10.42	1.6E-01	AF165860.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3648	16592	29607	1.2	1.6E-01	AJ003165.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3648	16592	29608	1.2	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABIS gene
3786	16827	29734	0.78	1.6E-01	AE000962.1	NT	Populus trichocarpa cv. Trichobel ABIS gene
4028	17063		2.81	1.6E-01	AE004413.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4356	17393	30265	10.43	1.6E-01	AF176980.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4494	17509		3.1	1.6E-01	AW966501.1	EST_HUMAN	Homo sapiens splein gene, complete cds
4494	17509		3.1	1.6E-01	AW966501.1	EST_HUMAN	EST1380777 MAGC resequencing, MAGJ Homo sapiens cDNA
4616	17933	30824	1.43	1.6E-01	Z28530.1	NT	Mus musculus chaperonin subunit 3 (gamma) (Ccp3), mRNA
4916	17933	30825	1.43	1.6E-01	Z28530.1	NT	S cerevisiae chromosome XI reading frame ORF YKR105c
4982	17997	30895	4.36	1.6E-01	AA098343.1	EST_HUMAN	S cerevisiae chromosome XI reading frame ORF YKR105c
5004	18018	30906	1.94	1.6E-01	AJ006356.1	NT	Z84H09.s1 Sitagliptin codon (8637204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TRE221955
5004	18018	30908	1.94	1.6E-01	AJ006356.1	NT	E221955 38 895 BP SEGMENT OF CHROMOSOME XIV. ; Lycopodium obscurum Real fragment 2, satellite region
5004	18018	30908	1.94	1.6E-01	AJ006356.1	NT	Lycopodium obscurum Real fragment 2, satellite region



Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5089	18079	30860	1.16	1.0E-01	BE019707.1	EST_HUMAN	Bab308.v1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3049023 5' similar to gb:M61715
5481	18563	31475	0.87	1.0E-01	L40808.1	NT	TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:X89857 M.musculus (MOUSE); Plasmidium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5500	18596	31686	2.82	1.0E-01	AW197466.1	EST_HUMAN	XM3301.1x1 NCI CGAP GC68 Homo sapiens cDNA clone IMAGE:2686959 3' similar to TR:075984 075984 HYPOTHETICAL 127.6 KD PROTEIN ;
5500	18596	31687	2.82	1.0E-01	AW197466.1	EST_HUMAN	XM3301.1x1 NCI CGAP GC68 Homo sapiens cDNA clone IMAGE:2686959 3' similar to TR:075984 075984 HYPOTHETICAL 127.6 KD PROTEIN ;
5612	18708	31965	2.31	1.0E-01	AF034716.1	NT	Rattus norvegicus COAATenhancer binding protein epsilon (cbpe) gene, complete cds
6144	19219	32449	0.9	1.0E-01	BE925803.1	EST_HUMAN	RC3-BN0034-370800-113-H01 BN0034 Homo sapiens cDNA
6395	19453	32697	0.57	1.0E-01	BF183584.1	EST_HUMAN	601809725R1 NIH_MGC 18 Homo sapiens cDNA clone IMAGE:4040335 3'
6395	19453	32698	0.57	1.0E-01	BF183584.1	EST_HUMAN	601809725R1 NIH_MGC 18 Homo sapiens cDNA clone IMAGE:4040335 3'
6508	19628	32893	1.98	1.0E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6508	19628	32894	1.99	1.0E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6950	20174	33498	0.55	1.0E-01	AA398047.1	EST_HUMAN	Human sapiens mRNA for KIAA1566 protein, partial cds
6959	20192	33519	0.65	1.0E-01	AB046796.1	EST_HUMAN	UHH-BE2-egl-b-06-Q-U1.51 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7156	18388	31232	4.63	1.0E-01	AW261216.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR132v
7518	20483	33644	0.61	1.0E-01	Z46632.1	NT	2822248 Spmme NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2822248 5'
8056	20993	34390	1.59	1.0E-01	AW246059.1	EST_HUMAN	Mus musculus Cdc-2>-dependent activator protein for secretion (Cadsps), mRNA
8090	21026	34425	0.57	1.0E-01	6759237	NT	AU136525 PLACE1 Homo sapiens cDNA clone IMAGE:1004468 5'
8102	21038	34425	1.15	1.0E-01	AU136525.1	EST_HUMAN	Cailla gorilla androgen receptor gene, partial exon
8201	21171	34582	1.28	1.0E-01	L40849.1	NT	TCBAP1E0607 Pediatric p16-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
8359	21328		0.51	1.0E-01	BE244087.1	EST_HUMAN	Bacteroides vulgatus beta-lactamase (cba) gene, complete cds and mobilization protein (mobA) gene, complete cds
8456	21425	34841	0.69	1.0E-01	U38243.1	NT	Bacillus subtilis complete genome (section 18 of 21); from 2997771 to 3213410
8978	21945	35359	0.85	1.0E-01	Z99119.1	NT	X60H08.r1 Scoville infant brain INIB Homo sapiens cDNA clone IMAGE:28873 5'
9178	22144	35571	0.71	1.0E-01	R13673.1	EST_HUMAN	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9295	22251		0.63	1.0E-01	L36861.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
9322	22287	35717	1.9	1.0E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
9466	22430		0.63	1.0E-01	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds, cfas gene, complete cds; and unknown gene
10039	22936		2.05	1.0E-01	BF37517.1	EST_HUMAN	RC3-S70200-041198-011-H01 S10200 Homo sapiens cDNA
10012	22959	36404	2	1.0E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
10048	22975		0.96	1.0E-01	BE155684.1	EST_HUMAN	PM2470353-270100-004-R11 T03553 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11017	23082	37609	2.89	1.6E-01	AW850653.1	EST_HUMAN	IL3-CT020-11189-028-G01 CT0220 Homo sapiens cDNA
11122	24082	37607	1.82	1.6E-01	Z28073.1	NT	S.cerevisiae chromosome XI reading frame ORF_YKL073w
11122	24082	37608	1.82	1.6E-01	Z28073.1	NT	S.cerevisiae chromosome XI reading frame ORF_YKL073w
11324	24284	37820	1.5	1.6E-01	BE258649.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11451	24394		3.84	1.6E-01	AF106064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3), complete cds
11440	24623	38204	6.89	1.6E-01	8671552.1	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
12155	25806		1.78	1.6E-01	6679468	NT	Mus musculus protein kinase, cGMP-dependent, type II (Pkg2), mRNA
12275	25995	38179	8.75	1.6E-01	AV718958.1	EST_HUMAN	AV718958 GLC Homo sapiens cDNA clone GI_CEMF07 6'
12608	26307		1.82	1.6E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-H01_1 LT0074 Homo sapiens cDNA
12697	26721		22.15	1.6E-01	AB045310.1	NT	Gucunis sativus KS mRNA for anti-keurone synthase, complete cds
12856	26463		2.73	1.6E-01	AK024498.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12945	25524		2.56	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosome protein S10 gene, partial cds; nuclear gene for mitochondrial product
12971	25537	31716	2.24	1.6E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
12978	25543		1.93	1.6E-01	BE287894.1	EST_HUMAN	601128459F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3346038 5'
248	13345	26270	1.73	1.6E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
248	13345	26271	1.73	1.6E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
589	15813		2.4	1.6E-01	AV711896.1	EST_HUMAN	AV711896 DCA Homo sapiens cDNA clone DCAADH06 5'
783	13343	26788	1.51	1.6E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1094	14138	27089	1.01	1.6E-01	AJ009735.1	NT	Oryzias latipes mRNA for EGG522 myosin heavy chain, 3UTR
1095	14143	27093	2.55	1.6E-01	AJ251885.1	NT	Homo sapiens partial SL C22A2 gene for organic cation transporter (OCT2), exon 1
1115	14169		1.57	1.6E-01	U36126.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1280	14315	27276	3.98	1.6E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1280	14315	27277	3.98	1.6E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1478	14511	27487	2.94	1.6E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1), mRNA, complete cds
1723	14847	27943	1.95	1.6E-01	AW444451.1	EST_HUMAN	U1H.B3-9b-b-99-q.U1.81 NC1 CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735641 3'
2723	15717	28736	1.47	1.6E-01	BF065361.1	EST_HUMAN	602883269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3247837 5'
2924	15882		1.1	1.6E-01	AW572516.1	EST_HUMAN	xy58a02.x2 NC1 CGAP_Pant1 Homo sapiens cDNA clone IMAGE:3247837 5'
3048	16105	28016	0.76	1.6E-01	M81441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN); Basal factor V variant 2 (factor V) mRNA, complete cds
3363	16413	29338	5.95	1.6E-01	AA035049.1	EST_HUMAN	cos8405.at NC1 CGAP_GC4 Homo sapiens cDNA clone IMAGE:1671337 3' similar to gb:M11453
3381	16430	29357	0.74	1.6E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN); L. signalin mRNA for G protein-coupled receptor
3381	16430	29358	0.74	1.6E-01	Z23104.1	NT	L. signalin mRNA for G protein-coupled receptor

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3440	16487	29405	0.97	1.5E-01	AW612237.1	EST_HUMAN	h22902.2 NCI, CGAP, Lu24 Homo sapiens cDNA clone IMAGE:2866339 3' similar to contains element
3768	16810	29719	2.22	1.5E-01	U09664.1	NT	NER16 repetitive element;
3782	16823	29731	0.8	1.5E-01	7108358	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3795	16835	29740	0.68	1.5E-01	M97882.1	NT	arabin, mRNA
3801	16920	29826	2.25	1.5E-01	AW665983.1	EST_HUMAN	XYNA, Thermobacterium; xynA, 4182 base-pairs
3808	16938	29846	0.71	1.5E-01	AJ003165.1	NT	H10106.x1 Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2861411 3'
3806	16938	29847	0.71	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal AB13 gene
4080	17115	30011	2.53	1.5E-01	AW366569.1	EST_HUMAN	Populus trichocarpa cv. Trichobal AB13 gene
4213	17242	30127	9.83	1.5E-01	AL163284.2	NT	RC2-HT0149-191098-012-009 H10149 Homo sapiens cDNA
4513	17538	30422	0.91	1.5E-01	BE791253.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
4513	17538	30423	0.91	1.5E-01	BE791253.1	EST_HUMAN	601583968F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938345 5'
4766	17776	30672	1.88	1.5E-01	BF687665.1	EST_HUMAN	601583968F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938345 5'
4783	15717	28735	2.86	1.5E-01	BF683391.1	EST_HUMAN	602067192F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:406223 5'
4830	17847	30748	1	1.5E-01	BE173798.1	EST_HUMAN	602067192F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4247537 5'
5034	18048	30828	1.2	1.5E-01	AL161560.2	NT	Homo sapiens cDNA
5134	18143	31023	1.07	1.5E-01	5579481	NT	CMO-HT0565-280200-245-510 HT0565 Homo sapiens cDNA
5328	18434	31185	2.46	1.5E-01	P07398	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
5357	18482	31331	1.03	1.5E-01	AF266852.1	NT	Homo sapiens calbindin 1, (28kd) (CALB1), mRNA
5401	18504		5.5	1.5E-01	P15196	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5616	18712	31870	4.35	1.5E-01	AW850754.1	EST_HUMAN	Calman oocodius MHC class II beta chain (hclbeta) gene, complete cds
5689	18755	31922	7.17	1.5E-01	U65016.1	NT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TES TIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5689	18755	31922	7.17	1.5E-01	U65016.1	NT	IL3-CT0219-150200-064-F10 CT0219 Homo sapiens cDNA
6012	19095	32295	0.79	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
6120	19198	32422	1.74	1.5E-01	6753659	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
6120	19198	32423	1.74	1.5E-01	6753659	NT	Mus musculus sodium channel, voltage-gated, type VI, alpha polypeptide (SCN6A) mRNA
6181	19236	32487	1.95	1.5E-01	AL278505.1	EST_HUMAN	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6319	19390	32630	3.25	1.5E-01	BE176858.1	EST_HUMAN	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6375	19443		1.86	1.5E-01	4506398	NT	Mus musculus genomic fragment, 270 Kb, chromosome 7
							601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3933981 5'
							Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6478	19543	32791	1.7	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds, and neuraminidase gene, partial cds
6601	25964	32985	1.8	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6681	19738	33013	4.63	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
6692	19749	33026	1.8	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6740	19766	33076	2.35	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6842	18895	33189	0.85	1.5E-01	AA714760.1	EST_HUMAN	nm00470.1 NCI CGAP GC80 Homo sapiens cDNA clone IMAGE:1241974.3
6871	18924	33220	1.8	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7171	18402	31247	6.15	1.5E-01	AW970295.1	EST_HUMAN	EST332376 MAGE resequences, MAGE Homo sapiens cDNA
7214	25578		0.71	1.5E-01	AA811545.1	EST_HUMAN	cb3302.81 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1337019.3 similar to contains element LTR2 repetitive element:
7424	20391	33945	1.91	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7621	20691	33945	1.68	1.5E-01	AF973157.1	EST_HUMAN	wf52008.x1 NCI CGAP U11 Homo sapiens cDNA clone IMAGE:2491310.3
7846	20763	34168	0.96	1.5E-01	AF298073.1	NT	Hos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7846	20783	34170	0.96	1.5E-01	AF298073.1	NT	Hos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7857	20802	34177	1.84	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BND-alk-4-05-Q-UJr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409.5
7857	20802	34178	1.84	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BND-alk-4-05-Q-UJr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409.5
8014	20952	34346	0.71	1.5E-01	U46560.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of fast-1 (SOL3) gene, complete cds
8393	21362	34769	1.21	1.5E-01	P21303	SWISSPROT	MEROZOTIE RECEPTOR PK68 PRECURSOR (68 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8562	21530	34950	0.97	1.5E-01	AA970317.1	EST_HUMAN	cd85g12.at NCI CGAP K465 Homo sapiens cDNA clone IMAGE:1573030.3 similar to gb:M26062
8555	21923		1.01	1.5E-01	BE884799.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8743	21711		13.33	1.5E-01	C16800.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004.5
8776	21743	35165	1.60	1.5E-01	L27835.1	NT	C16800 Clontech human apta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-528-H09.5
8940	21908	35330	1.79	1.5E-01	D84478.1	NT	Pargasinodon gigas growth hormone (GH) mRNA, complete cds
8962	21928		0.74	1.5E-01	P13446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
9180	22166	35595	1.31	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
9460	22424	35982	3.06	1.5E-01	N74228.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9548	22511	35980	1.03	1.5E-01	BF585465.1	EST_HUMAN	zaf59e06.s1 Soares fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:268868.3 similar to
9555	22517		2.73	1.5E-01	AF754819.1	EST_HUMAN	PIR-S44443 S44443 RAD23 protein homolog2 - human;
9760	22701		0.87	1.5E-01	AU130007.1	EST_HUMAN	GV0000494 Human Podiatia Differential Display Homo sapiens cDNA
9808	21131	34634	6.92	1.5E-01	U00456.1	NT	AA7754819 TP Homo sapiens cDNA clone TPAAHB12.5
			0.92	1.5E-01	AU130007.1	EST_HUMAN	AU730007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080.5
			6.92	1.5E-01	U00456.1	NT	Acipenser transmontanus vitellogenin mRNA, partial cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10176	23101	36581	0.58	1.5E-01	M17144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
10261	23206	36590	6.22	1.5E-01	AJ007570.1	NT	Apysia californica carboxypeptidase D mRNA, complete cds
10261	23206	36591	8.22	1.5E-01	AJ007570.1	NT	Apysia californica carboxypeptidase D mRNA, complete cds
10583	23485	36979	2.87	1.5E-01	X98652.1	NT	P. lentisculus mRNA for integrin beta subunit
10651	23573		0.52	1.5E-01	AB027759.1	NT	Mesocricetus auratus mRNA for collagen type XVII, complete cds
10671	23593	37089	2.49	1.5E-01	AB14046.1	EST_HUMAN	wk53112.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10671	23593	37090	2.49	1.5E-01	AB14046.1	EST_HUMAN	wk53112.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10753	23575	37172	2.19	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax6b (Pax6) mRNA, complete cds
10906	23826	37338	2.14	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10906	23826	37339	2.14	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
11173	24130	37669	4.35	1.5E-01	AL05280.2	NT	Homo sapiens chromosome 21 segment HS21Q680
11173	24130	37669	4.35	1.5E-01	AL05280.2	NT	Homo sapiens chromosome 21 segment HS21Q680
11412	24356	37891	1.71	1.5E-01	AW841915.1	EST_HUMAN	IL5-ON0024-03030-025-D04 ON0024 Homo sapiens cDNA clone IMAGE:773091 5' similar to contains element MER22 repetitive element;
11449	24392	37937	3.96	1.5E-01	AA425488.1	EST_HUMAN	zvl66002.1 Soares, total fetus N123-F6_3w Homo sapiens cDNA clone IMAGE:2491310 3'
11501	20561	33945	1.69	1.5E-01	AJ973157.1	EST_HUMAN	wf52008.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2485549 5'
12259	25769		11.17	1.5E-01	BF700562.1	EST_HUMAN	602128753.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:2485549 5'
12607	25306		1.82	1.5E-01	AF030358.2	NT	Rattus norvegicus ctenodine CX3C mRNA, complete cds
12610	25309		1.81	1.5E-01	AJ236332.1	NT	Mus musculus mRNA for death inducer-obitator-1 (Dio-1)
12668	25761		12.47	1.5E-01	R63077.1	EST_HUMAN	yp7404.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194430 5'
12748	25814		2.45	1.5E-01	AJ741272.1	EST_HUMAN	AV741272 CG Homo sapiens cDNA clone CBDA004 5'
12855	25722	31613	7.87	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCT C11168 complete genome, segment 1/6
13073	25606	31689	1.53	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
269	13393		2.07	1.4E-01	AF009683.1	NT	Homo sapiens T cell receptor beta locus, TORBVS6P to TORBV21S2A2 region
911	13966		3.95	1.4E-01	D76538.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1264	14299		2.77	1.4E-01	T91864.1	EST_HUMAN	yp5400.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112032 3'
1763	14792		1.61	1.4E-01		EST_HUMAN	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1768	14795	27780	1.82	1.4E-01	AE001710.1	NT	Thermidolia maritima segment 22 of 136 of the complete genome
2002	15023		12.82	1.4E-01	AA720615.1	EST_HUMAN	nv72007.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1285821 3'
2482	15486	28509	1.15	1.4E-01	P30706	SWISSPROT	GLYCEOL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2804	15796	28616	7.57	1.4E-01	A893466.1	EST_HUMAN	wn7440.1.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'

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Table 4

### Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3914	16954	29885	0.93	1.4E-01	R59232.1	EST_HUMAN	y997a03.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:41487 5'
3914	16954	29886	0.93	1.4E-01	R59232.1	EST_HUMAN	y997a03.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:41487 5'
3914	16954	29886	0.93	1.4E-01	R59232.1	EST_HUMAN	y997a03.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:41487 5'
4202	17233	30120	11.04	1.4E-01	AI690094.1	EST_HUMAN	x56502.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4202	17233	30120	11.04	1.4E-01	AI690094.1	EST_HUMAN	x56502.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4202	17233	30120	11.04	1.4E-01	AI690094.1	EST_HUMAN	x56502.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4265	17294	30173	3.96	1.4E-01	AE001710.1	NT	Thermatopha maritima clone 22 of 130 of the complete genome
4265	17294	30173	3.96	1.4E-01	AE001710.1	NT	Thermatopha maritima clone 22 of 130 of the complete genome
4440	17466		0.71	1.4E-01	AA775287.1	EST_HUMAN	z350b01.s1 Soares fetal liver spleen. 1N1S.S1 Homo sapiens cDNA clone IMAGE:453873 3' similar to gb:X01057.nm1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN) contains Alu repetitive element
4703	17724	30618	0.89	1.4E-01	S453861	NT	Homo sapiens phosphodiesterase 4A, cAMP-specific (Drosophila)-homolog phosphodiesterase E(2) (PDE4A), mRNA
4807	17924	30817	0.92	1.4E-01	AV686959.1	EST_HUMAN	AV686959 GKC Homo sapiens cDNA clone GKCDUG09 5'
5379	18483	31358	4.72	1.4E-01	T09077.1	EST_HUMAN	y016c11.s1 Stragelung Lung (9337210) Homo sapiens cDNA clone IMAGE:117812 3'
5402	18505	31381	4.06	1.4E-01	AB004558.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5402	18505	31382	4.06	1.4E-01	AB004558.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6430	19496	32749	2.9	1.4E-01	BE326891.1	EST_HUMAN	h87d02.x1 NCL CGAP_Kid17 Homo sapiens cDNA clone IMAGE:3133638 3'
6629	19687	32965	5.1	1.4E-01	AU111747.1	EST_HUMAN	AU111747 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6629	19687	32966	5.1	1.4E-01	AU111747.1	EST_HUMAN	AU111747 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6723	19779	33058	3.48	1.4E-01	AW082766.1	EST_HUMAN	x47d1d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
6737	19793		1.28	1.4E-01	BE266536.1	EST_HUMAN	QV1-UM0036-383305-103-409 UM0036 Homo sapiens cDNA
6759	19813	33093	0.74	1.4E-01	BF378633.1	EST_HUMAN	DKFZp761A0910.1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5'
7333	20304		0.74	1.4E-01	AL118563.1	EST_HUMAN	U4-H-BIO-aak-c-094.01 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7615	20376		1.87	1.4E-01	AW016373.1	EST_HUMAN	HSC1D0011 normalized Infant brain cDNA Homo sapiens cDNA clone c-1db01
7841	20501	33066	0.91	1.4E-01	F08745.1	EST_HUMAN	w04f12.1 NCL CGAP_CL1 Homo sapiens cDNA clone IMAGE:2389285 3' similar to SW1CE4_HUMAN
7894	20552		0.81	1.4E-01	AW52827.1	EST_HUMAN	P49692 CASPASE-4 PRECURSOR
7883	20527	34203	0.92	1.4E-01	U85645.1	NT	Oryctolagus cuniculus fructose 1,6-bisphosphate aldolase (AldB) gene, complete cds
8029	20666	34361	1.24	1.4E-01	AI305192.1	EST_HUMAN	q80b172.x1 Soares_NHMPUL_S1 Homo sapiens cDNA clone IMAGE:1876583 3'
8818	21785		1.24	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCF5H06 3'
9136	22102		0.87	1.4E-01	AI436093.1	EST_HUMAN	h82d12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128111 3' similar to TR:002710.002710 GAG POLYPROTEIN
9244	22230	35681	4.86	1.4E-01	AI307073.1	EST_HUMAN	DI8B03.y1 Martin Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9346	22310	35735	0.95	1.4E-01	AW023636.1	EST_HUMAN	y10h05.r1 Soares placenta N24PH Homo sapiens cDNA clone IMAGE:138873 5'
9478	22442	35883	0.94	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta N24PH Homo sapiens cDNA clone IMAGE:138873 5'
9478	22442	35884	0.94	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta N24PH Homo sapiens cDNA clone IMAGE:138873 5'

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9841	22804	35983	9.19	1.4E-01	BF310669.1	EST_HUMAN	601695465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9830	22874	36024	1.19	1.4E-01	W93411.1	EST_HUMAN	g93404.1 Scores fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element:
9702	22655	36109	0.43	1.4E-01	X73283.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9702	22655	36110	0.43	1.4E-01	X73283.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9713	22666	36123	1.44	1.4E-01	Y10166.1	NT	Homo sapiens PHX gene
9713	22666	36124	1.44	1.4E-01	Y10166.1	NT	Homo sapiens PHX gene
9805	21128	34532	2.06	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ia (IAL), and zinc finger protein (DNZ1) genes, complete cds
10164	23089	36587	0.55	1.4E-01	X66082.1	NT	C.perfringens ORF for putative membrane transport protein
10346	23370	36747	1.12	1.4E-01	AF023813.1	NT	Macromitrium levetum small ribosomal protein 4 (ps4) gene, chloroplast gene encoding chloroplast protein, partial cds
10448	23370	36661	0.57	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2465094 5'
10448	23370	36662	0.57	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2465094 5'
10619	23541	37039	0.67	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211289-013-008 ST0218 Homo sapiens cDNA
10619	23541	37040	0.67	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211289-013-008 ST0218 Homo sapiens cDNA
10629	23750		0.56	1.4E-01	T84283.1	EST_HUMAN	y476d03.1 Scores fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:111386 5'
10962	23882	37395	0.71	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 259451 to 2812870
11191	24147	37680	2.89	1.4E-01	R63400.1	EST_HUMAN	Y70c05.1 Scores breast 2NbH8at Homo sapiens cDNA clone IMAGE:154088 5'
11432	24376	37916	2.53	1.4E-01	P08648	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-5) (VLA-5) (CD49E)
11752	24637		1.59	1.4E-01	AL161496.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 8
11797	23952	37474	2.38	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), inosophosphate isomerase (TPI) genes, complete cds
11955	24737		1.55	1.4E-01	X82102.1	NT	M.musculus p16K gene for 16 kDa protein
12548	25272	31776	2.33	1.4E-01	X74773.1	NT	P.salina Placid gene sacY
12562	25280		2.24	1.4E-01	11988117	NT	Rattus norvegicus desmin (Des), mRNA
12905	25964		2.35	1.4E-01	BE613802.1	EST_HUMAN	601315638F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3634329 5'
12702	25362		4.86	1.4E-01	D64004.1	NT	Synochysis sp. PC06803 complete genome, 23127, 28697-3002865
12776	25681		4.86	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12998	25792		3.72	1.4E-01	D82863.1	NT	Mus musculus mRNA for prolidase, complete cds
13067	25601		2.63	1.4E-01	AW377698.1	EST_HUMAN	MRQ-HT0208-221296-204-c08 HT0208 Homo sapiens cDNA
322	13414	26338	2.48	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
322	13414	26339	2.48	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA

Table 4  
Single Exon Probes Expressed in Bone Marrow.

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
530	13601	28519	2.91	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
637	13703	28624	0.78	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/93UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93UK
637	13703	28625	0.78	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/93UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93UK
845	13701	28830	1.04	1.3E-01	X63330.1	NT	P. dumetii histone gene cluster for core histones H2A, H2B, H3 and H4
895	13950	28908	1.76	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1028	14074	27024	1.8	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1129	14172		2.88	1.3E-01	AL116263.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1220	14288	27215	1.51	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF05.5
1438	14471		0.93	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1476	14897	27989	2.07	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2180	15195		1.69	1.3E-01	AJ243578.1	NT	Rhodospirillum rubrum acd1001 pucB5, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF1.51
2298	16310		0.96	1.3E-01	AW812104.1	EST_HUMAN	RCA-ST0173-191099-032-412 ST0173 Homo sapiens cDNA
2389	16307		3.94	1.3E-01	AE001018.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2592	16593	28810	2.23	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3465	16511	29432	0.98	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydroxyol transacylase mRNA, complete cds
3735	16771	29689	0.91	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3735	16771	29690	0.91	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3741	16783	29695	0.89	1.3E-01	AS032158.1	NT	Homo sapiens DD4 gene for dihydrodiphenylase 4 [AKR TC4], exon 2
3794	16777	29689	0.67	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3794	16777	29690	0.67	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3816	16856	29762	0.74	1.3E-01	6978940	NT	Rattus norvegicus Fibronectin, gamma polypeptide (Fg), mRNA
4014	17053		1.48	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, centig fragment No. 77
4081	13703	28624	7.11	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/93UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93UK
4081	13703	28625	7.11	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/93UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93UK
4163	17194		1.12	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4185	17216		4.1	1.3E-01	AF036341.1	EST_HUMAN	QV3-DT0018.081289-038-033 DT0018 Homo sapiens cDNA
4194	17226	30114	2.47	1.3E-01	AF026803.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4215	17244	30129	20.19	1.3E-01	AW273741.1	EST_HUMAN	XV23110.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995.3
4343	17370		1.49	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C090



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4505	17630	30414	0.8	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydroxyol transacylase mRNA, complete cds
4594	17587	30476	2.72	1.3E-01	BE272339.1	EST_HUMAN	601126006F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:2960063 5'
5014	18028		0.91	1.3E-01	AU135619.1	EST_HUMAN	AU135619 PLACE1 Homo sapiens cDNA clone IMAGE:1004663 5'
5060	18070		0.63	1.3E-01	BF031980.1	EST_HUMAN	RCA-TN0077-180900-012-c05 TN0077 Homo sapiens cDNA
5398	18501	31379	0.76	1.3E-01	AW469888.1	EST_HUMAN	ha076065.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1
5436	18533	31446	1.98	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0093-100-00-188-a08 UM0093 Homo sapiens cDNA
5579	18673		0.91	1.3E-01	AF107783.1	NT	Emmericella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5655	18760		0.88	1.3E-01	AF056880.1	NT	Hepatitis C virus 68_Q.10 genome polyprotein gene, partial cds
5813	18803	32066	0.95	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6099	19178	32396	0.98	1.3E-01	BF527281.1	EST_HUMAN	602036337F2 NCI_CGAP_Bln67 Homo sapiens cDNA clone IMAGE:4177233 5'
6099	19178	32397	0.98	1.3E-01	BF527281.1	EST_HUMAN	602036337F2 NCI_CGAP_Bln67 Homo sapiens cDNA clone IMAGE:4177233 5'
6630	19696	32967	17.29	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6720	19776	33055	2.08	1.3E-01	X88891.1	NT	C. jacchus intron 4 of visual pigment gene (not allele)
6940	20164	33467	0.94	1.3E-01	H73425.1	EST_HUMAN	yu02401.r1 Soares fetal liver spleen 1NF.LS Homo sapiens cDNA clone IMAGE:282609 5'
6955	20180		0.82	1.3E-01	W26367.1	EST_HUMAN	2853 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7009	20135	33450	1.04	1.3E-01	BE783926.1	EST_HUMAN	601469667F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866079 5'
7009	20135	33451	1.04	1.3E-01	BE783926.1	EST_HUMAN	601469667F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866079 5'
7211	20234		0.72	1.3E-01	BF526550.1	EST_HUMAN	602044345F1 NCI_CGAP_Bln67 Homo sapiens cDNA clone IMAGE:4181866 5'
7477	20443		2.15	1.3E-01	H48654.1	EST_HUMAN	y333402.r1 Soares fetal liver spleen 1NF.LS Homo sapiens cDNA clone IMAGE:207075 5'
8292	21261		0.97	1.3E-01	BE272339.1	EST_HUMAN	601126006F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:2960063 5'
8306	21275	34696	1.59	1.3E-01	11423284	NT	Homo sapiens PRO0611 protein (PRC0611), mRNA
8335	21305	34720	1.18	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4296074 3'
8580	21548		0.66	1.3E-01	BE562528.1	EST_HUMAN	601335629F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3686934 5'
8617	21585	35001	0.6	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8688	21656		4.88	1.3E-01	Z74102.1	NT	S. cerevisiae chromosome IV reading frame ORF YD054c
8729	21697		4.2	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A.2 (MACROH2A2), mRNA
8873	21840	35263	1.05	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4296074 3'
9300	22265	35694	0.55	1.3E-01	R11172.1	EST_HUMAN	y33911.r1 Soares fetal liver spleen 1NF.LS Homo sapiens cDNA clone IMAGE:129284 5' similar to
9300	22265	35695	0.55	1.3E-01	R11172.1	EST_HUMAN	SP-RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9574	22536	35967	0.65	1.3E-01	11058003	NT	SP-RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9574	22536	35968	0.65	1.3E-01	11058003	NT	Plutella lycaletalis granulovirus, complete genome

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9827	22876	36132	3.9	1.3E-01	AF023126.1	NT	Oryzobolus curvulus H <sup>+</sup> K-A TPase alpha 2c subunit mRNA, complete cds
10129	23055		0.74	1.3E-01	N86348.1	EST_HUMAN	J7937F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7937 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10411	23333		0.89	1.3E-01	5339940	NT	Rattus norvegicus peptidyl arginine diaminase, type IV (P-d4), mRNA
10489	23411	36908	0.88	1.3E-01	AW851599.1	EST_HUMAN	MR2-C10222-201058-001-e01 C10222 Homo sapiens cDNA
10757	25702	37173	1.08	1.3E-01	AL105246.2	NT	Homo sapiens chromosome 21 segment HS27C046
10891	23811	37318	0.66	1.3E-01	AU121287.1	EST_HUMAN	AU121287 HEMBB1 Homo sapiens cDNA clone HEMBB 1002387 5'
10956	23856	37372	0.45	1.3E-01	AW247836.1	EST_HUMAN	2820637.3prime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2820637 3'
10986	23902		2.57	1.3E-01	BF330999.1	EST_HUMAN	MR4-B10358-130700-010-H08 B10358 Homo sapiens cDNA
11581	24519		3.56	1.3E-01	5871745	NT	Mus musculus collagen 2, muscle (CR2), mRNA
11670	24606	38182	1.77	1.3E-01	AW082636.1	EST_HUMAN	xc2008.xt NCL CGAP_C018 Homo sapiens cDNA clone IMAGE:2584841 3'
11670	24606	38183	1.77	1.3E-01	AW082636.1	EST_HUMAN	xc2008.xt NCL CGAP_C019 Homo sapiens cDNA clone IMAGE:2584841 3'
11922	24603	38395	2.33	1.3E-01	BE279449.1	EST_HUMAN	901188052F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3504804 5'
12397	25171	31817	1.83	1.3E-01	BE618346.1	EST_HUMAN	901482741F1 NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3866003 5'
12535	25250		3.3	1.3E-01	AL242790.1	NT	Gallus gallus scp1 gene for lymphotactin, exons 1-3
12692	25357	31766	1.37	1.3E-01	BF572303.1	EST_HUMAN	90207753F1 NIH_MGC 82 Homo sapiens cDNA clone IMAGE:4252082 5'
12885	25475		1.48	1.3E-01	AB028808.1	NT	Ephyraida fuvestilis mRNA for sALK-8, complete cds
12915	25494		2.52	1.3E-01	AW001114.1	EST_HUMAN	TR-O60287 O60287 KIA00539 PROTEIN ;
383	13466	26428	14.65	1.2E-01	AA421744.1	EST_HUMAN	139402.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gbl:U02760_rna1
424	13119		1.38	1.2E-01	U68912.1	NT	ANNEXIN V (HUMAN);
548	13619		2.78	1.2E-01	AF039442.1	NT	Dicoryphum dicoryphum ORF DG1016 gene, partial cds
1377	14411	27381	2.19	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1377	14411	27382	2.19	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1383	14417		4.88	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1388	14421		0.92	1.2E-01	AL445066.1	NT	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1507	14540		1.23	1.2E-01	AA897474.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1635	14687	27643	1.82	1.2E-01	Q14934	SWISSPROT	Thermolobitis acidophilum complete genome, segment 4/5
1658	14690	27668	2.99	1.2E-01	AI265402.1	EST_HUMAN	ak6809.at Scores_NFL_C03 S1 Homo sapiens cDNA clone IMAGE:1460594 3' similar to Tr:Q16571
1783	14812		18.89	1.2E-01	X89211.1	NT	Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR ;
1934	14938		1.76	1.2E-01	AW445068.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
							UHH-B18-aid-a-10-Q-U1.at NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2163	15208	28227	1.66	1.2E-01	BF249480.1	EST_HUMAN	g01821567f1 NIH_MGC. 62 Homo sapiens cDNA clone IMAGE:4046224 5'
2294	15308	28329	1.21	1.2E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2595	15596	28614	2.05	1.2E-01	AW1969556.1	EST_HUMAN	QV3-BN0046-220300-126-f10 BN0046 Homo sapiens cDNA
2802	15802	28624	1.61	1.2E-01	BE216686.1	EST_HUMAN	h65604.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178303 3'
2738	15732	28748	37.59	1.2E-01	AB233388.1	EST_HUMAN	ist8907.x1 NCI_CGAP_Pant Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] contains element PTR5 repetitive element;
2855	15915	28938	1.4	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-P) mRNA, partial cds
2913	15971	28995	2.03	1.2E-01	AI720470.1	EST_HUMAN	ss80409.x1 Barstead cdon HPI_R97 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb.L05095
2946	16004	28929	2.52	1.2E-01	MI6384.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
3017	16075	28998	0.73	1.2E-01	X59882.1	NT	Human creatine kinase-B mRNA, complete cds
3244	16289	28224	1.34	1.2E-01	AV370689.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3271	16325		0.82	1.2E-01	U67600.1	NT	QV1-B10265-281096-021-c05 B10265 Homo sapiens cDNA
3533	16578	29502	0.86	1.2E-01	X59882.1	NT	Methanococcus jannaschii scellon 142 of 150 of the complete genome
3533	16578	29503	0.86	1.2E-01	X59882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3620	16538		1.05	1.2E-01	Z89118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3760	16821	30125	0.7	1.2E-01	BF128551.1	EST_HUMAN	Basillus subtilis complete genome (section 16 of 21): from 2795131 to 3013540
4211	17240	30126	2.16	1.2E-01	Z54255.1	NT	g01810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053968 3'
4211	17240	30126	2.16	1.2E-01	Z54255.1	NT	P clarkii mRNA; repeat region (ID 2MRT7)
4751	17771	30687	0.98	1.2E-01	Z48183.1	NT	P clarkii mRNA; repeat region (ID 2MRT7)
5116	18126		1	1.2E-01	P16466	SWISSPROT	Lesosulfonium tRNA for glycylalase-1
5150	18159	31038	0.81	1.2E-01	AL163227.2	NT	HEMOLYSIN PRECURSOR
5150	18159	31039	0.91	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5164	18173	31052	1	1.2E-01	AL161516.2	NT	Homo sapiens chromosome 21 segment HS21C027
5234	18242	31114	0.81	1.2E-01	BE974502.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
5322	18428	31178	0.75	1.2E-01	AA744389.1	EST_HUMAN	h035004.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:3950711 3'
5373	18478	31351	0.91	1.2E-01	AF223391.1	NT	h035004.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
5383	18487	31361	2.27	1.2E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5442	18544	31458	2.15	1.2E-01	Z96286.1	EST_HUMAN	z008402.1 Soares parathyroid tumor NHAPA Homo sapiens cDNA clone IMAGE:321659 5'
5583	18643	31643	0.95	1.2E-01	Z46234.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
6324	19394	32639	2.66	1.2E-01	BE620445.1	EST_HUMAN	Mdomestica Borkh. Granmy Smith adh mRNA for alcohol dehydrogenase
6376	19444	32686	1.1	1.2E-01	P10842	SWISSPROT	h035004.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:3895613 5'
							MATING-TYPE P-SPECIFIC POLYPEPTIDE P1

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6431	19497	32750	2.19	1.2E-01	AW845275.1	EST_HUMAN	LOC70031-221099-119-64 CT0031 Homo sapiens cDNA
6499	19593	32815	1.38	1.2E-01	M28925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6804	19858	33145	0.89	1.2E-01	BF347895.1	EST_HUMAN	600202311271 NCL_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4159396 5'
6966	20190	33517	0.95	1.2E-01	AF295759.1	NT	JC virus antigen, VP2, VP3, VP1, large T antigen, and small t antigen genes, complete cds
7210	20233	33557	0.67	1.2E-01	H47789.1	EST_HUMAN	hp0004-11 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:193759 5'
7210	20233	33558	0.67	1.2E-01	H47789.1	EST_HUMAN	hp0004-11 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:193759 5'
7854	20799	34175	0.62	1.2E-01	AJ271741.1	NT	Homo sapiens partial ILF3 gene for Interleukin enhancer binding factor 3 (alternative transcript dbp76, dbp76 gamma, dbp76 alpha and ILF3)
8053	21000	34396	0.9	1.2E-01	BF880513.1	EST_HUMAN	602155195FT NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4286382 5'
8098	21034	34433	0.57	1.2E-01	D87458.1	NT	Human mRNA for KIAA0282 gene, partial cds
8098	21034	34434	0.57	1.2E-01	D87458.1	NT	Human mRNA for KIAA0282 gene, partial cds
8224	21193		1.24	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-009 BN0137 Homo sapiens cDNA
8295	21264	34675	3.1	1.2E-01	AB13753.1	EST_HUMAN	we99g03.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2328904 3' similar to SW7GST2_HUMAN
8341	21310	34724	0.76	1.2E-01	Q02369	SWISSPROT	Q99735 MICROSMAL GLUTATHIONE S-TRANSFERASE L1
8652	21620	35040	0.61	1.2E-01	AB83981.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX LB22) (CHB22)
8739	21707		10.85	1.2E-01	AW063652.1	EST_HUMAN	af7b10.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2377435 3'
							(HUMAN);
8789	21726		3.98	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8798	21765	35187	0.69	1.2E-01	J03955.1	NT	N. crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8798	21765	35188	0.69	1.2E-01	J03955.1	NT	N. crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8948	21914		0.81	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
9037	22003		2.01	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
9073	22039		0.64	1.2E-01	X15191.1	NT	M. musculus DNA fragment of Apolipoprotein B gene
9930	22813	36287	1.69	1.2E-01	X77861.1	NT	S. cerevisiae HXT5 gene
10395	23268	36765	1.84	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cui Homo sapiens cDNA clone CUAAKE08 5'
11232	24165		2.36	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11404	24348		2.55	1.2E-01	BE963324.2	EST_HUMAN	601655578RT NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3848283 3'
11482	24425		1.57	1.2E-01	BF314481.1	EST_HUMAN	601900765FT NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4130103 5'
11584	24532	38077	2.45	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAT1 (DNAT1) gene, exon 17
11738	24623	38201	1.6	1.2E-01	9994174	NT	Homo sapiens UDP-Gal:betaGalNAc beta 1,4-galactosyltransferase, polypeptide 4 (BAG14), mRNA

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar ("Top") Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11836	24718		1.54	1.2E-01	M65106.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12182	25016		3.86	1.2E-01	AV059003.1	EST_HUMAN	AV059003 GLC Homo sapiens cDNA clone GLC1B12 3'
12517	25248		2.78	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
12593	25922	31304	6.17	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RGN) (CDW138) (CD138 ANTIGEN)
12605	25432		2.86	1.2E-01	X53981.1	NT	R. norvegicus NF88 gene for 68kDa neurofilament
12687	25935	31310	1.38	1.2E-01	BE061418.1	EST_HUMAN	QV4-BT0234-111189-031-g10 BT0234 Homo sapiens cDNA
12899	25477	31731	9.82	1.2E-01	AI266803.1	EST_HUMAN	in20q05.x1 NCL CGAP_Lus Homo sapiens cDNA clone IMAGE:1898940 3'
12911	25490		2.91	1.2E-01	L0187.1	NT	Xenopus laevis histatin alpha 3 subunit mRNA, partial cds
12917	25862		9.28	1.2E-01	O96433	SWISSPROT	CYCLIN I
12946	25525	31712	1.76	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 88 of the complete chromosome
13092	16538		2.08	1.2E-01	Z59118.1	NT	Bacillus subtilis complete genome (section 15 of 21), from 2795131 to 3013540
13098	25623		1.5	1.2E-01	BF314481.1	EST_HUMAN	801900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
586	13636	26552	1.01	1.1E-01	AI861003.1	EST_HUMAN	in16a08.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'
617	13682	26569	1.84	1.1E-01	AA589006.1	EST_HUMAN	hmdg11.x1 NCL CGAP_Co10 Homo sapiens cDNA clone IMAGE:1069920 3' similar to gb-X06985_jna1
1057	14103	27054	1.55	1.1E-01	BF597308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1087	14131		1.48	1.1E-01	AL161580.2	NT	802128847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1163	15690	27158	4.8	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1254	14280	27255	2.03	1.1E-01	D64004.1	NT	EST1394142 MAGE sequences, MAGL Homo sapiens cDNA
1524	14566	27627	2.46	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2686767-3002965
2322	15333		2.72	1.1E-01	6755215	NT	AUT103683 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2545	15926		0.83	1.1E-01	6978878	NT	Mus musculus p16 T-cell antigen receptor alpha (Pctra) mRNA
2574	15575	28578	0.93	1.1E-01	AW821009.1	EST_HUMAN	Rattus norvegicus Procollagen II alpha 1 (Col2a1) mRNA
3046	15103	28017	0.95	1.1E-01	F05285.1	EST_HUMAN	RCO-ST0376-210100-332-d04 ST0376 Homo sapiens cDNA
3352	16403		1.66	1.1E-01	6753231	NT	HSCR1022 normalized infant brain cDNA Homo sapiens cDNA clone c-1fr02 3'
3432	16480	28389	2.18	1.1E-01	BE383186.1	EST_HUMAN	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3465	16512	28433	1.3	1.1E-01	X62135.1	NT	C. reinhardtii nuclear gene on linkage group XIX
3566	16641	28560	0.8	1.1E-01	Y07695.1	NT	A. thaliana gene for transposase
3715	16758		0.86	1.1E-01	P97384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN XI) (CAP-50)
3722	16765	28678	1.23	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4137	17169	30054	1.14	1.1E-01	AW819412.1	EST_HUMAN	MK3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4137	17169	30055	1.14	1.1E-01	AW819412.1	EST_HUMAN	MF3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4281	17310		9.36	1.1E-01	AF157066.1	NT	Drosophila melanogaster klarsicht protein (klx) mRNA, complete cds

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4316	17345	30226	0.99	1.1E-01	AW802056.1	EST_HUMAN	IL5-UM0070-020500-068-008 UM0070 Homo sapiens cDNA
4870	17891	30577	1.02	1.1E-01	S44657.1	NT	Tape-1 integral membrane protein TAPA-1 [Hicra, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4869	17896	30774	0.98	1.1E-01	Y07895.1	NT	Aluminae gene for transposase
5058	17174		0.76	1.1E-01	AF030001.1	NT	Male nucleolar major histocompatibility locus class III region: tyrophilin-like protein gene, partial cds; Nucle4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X(TNX) genes, complete
5753	18847		1.36	1.1E-01	AA747216.1	EST_HUMAN	nt76003.st NCI_CGAP_Ext1 Homo sapiens cDNA clone IMAGE:1289140 similar to contains Alu repetitive element/contains element MER35 repetitive element;
5828	18819	32102	1.16	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5898	18957	32145	0.95	1.1E-01	AL110985.1	NT	Bovine chondrocyte strain T4 cDNA library under conditions of nitrogen deprivation
5904	18990	32180	0.73	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4168818 5'
5904	18990	32181	0.73	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4168818 5'
5935	19021	32215	1.67	1.1E-01	X68951.1	NT	S pombe ssd gene encoding protein kinase
5971	18056	32256	4.98	1.1E-01	M86533.1	NT	Providencia reagent penicillin G amidase gene
6142	19217	32448	1.83	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6184	19239	32470	1.54	1.1E-01	BE786152.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
6184	19259	32463	8	1.1E-01	AY853690.1	EST_HUMAN	RC3-C10284-280998-011-401 C10284 Homo sapiens cDNA
6564	19624	32989	0.5	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS27C082
6571	19631	32998	1.26	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6617	19675	32953	0.84	1.1E-01	AJ216307.1	EST_HUMAN	q97806.st Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:1841089 3'
6762	19815	33095	6.18	1.1E-01	Q69935	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME)
6862	19915		2.81	1.1E-01	AF032822.1	NT	Homo sapiens synlexin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6862	20187	33512	2.23	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7249	19884	33281	0.65	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 96 of 99 of the complete genome
7249	19884	33282	0.65	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 96 of 99 of the complete genome
7363	25999		0.94	1.1E-01	BF382758.1	EST_HUMAN	6071816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050663 5'
7523	25983	33950	1.59	1.1E-01	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1186001-1485000 nt, position (67)
7781	20734	34103	7.89	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
7781	20734	34106	7.89	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
7839	20766	34161	0.54	1.1E-01	AA969008.1	EST_HUMAN	ou44903.st Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:1628172 3'
7917	20860	34248	1.77	1.1E-01	F41067	SWISSPROT	TRAB PROTEIN
7959	20900		0.79	1.1E-01	Z14098.1	NT	B subtilis gene encoding hypothetical polyketide synthase

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7981	20902	34294	2.99	1.1E-01	AA788784.1	EST_HUMAN	ek31106.s1 Soares_parenchymal_tumor_NHHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483 CHROMOGRAMIN A PRECURSOR (HUMAN);
8111	21048	34448	0.65	1.1E-01	BE782290.1	EST_HUMAN	801470056F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873228 5'
8301	21270	34882	0.48	1.1E-01	U67482.1	NT	Methanococcus jannaschii section 34 of 150 of the complete genome
8550	21518	34936	1.61	1.1E-01	AA489574.1	EST_HUMAN	rh04910.s1 NCI_CGAP_T1H1 Homo sapiens cDNA clone IMAGE:943362
8550	21518	34937	1.61	1.1E-01	AA489574.1	EST_HUMAN	rh04910.s1 NCI_CGAP_T1H1 Homo sapiens cDNA clone IMAGE:943362
8588	21568	34982	1.1	1.1E-01	X91233.1	NT	H.sapiens L15 gene
8937	21605		1.08	1.1E-01	AW817918.1	EST_HUMAN	PM1-ST0270-090200-001-09 ST0270 Homo sapiens cDNA
8984	21682	35088	1.59	1.1E-01	AL134349.1	EST_HUMAN	DKFZp547P184_T1 547 (synonym: hBr1) Homo sapiens cDNA clone DKFZp547P184 5'
9170	22136	35562	1.82	1.1E-01	U02482.1	NT	Podococcus acidilactici H plasmid pSMB74 peptidase ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds
9253	22228	35660	0.86	1.1E-01	A1807474.1	EST_HUMAN	wf4801.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element;
9332	22327	35756	0.56	1.1E-01	AF050091.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
9398	22363	35794	2.27	1.1E-01	AA162153.1	EST_HUMAN	z98312.r1 Stratiogene muscle 937209 Homo sapiens cDNA clone IMAGE:827743 5'
9398	22363	35795	2.27	1.1E-01	AA162153.1	EST_HUMAN	z98312.r1 Stratiogene muscle 937209 Homo sapiens cDNA clone IMAGE:827743 5'
9480	22454	35894	0.77	1.1E-01	Y12727.1	NT	P.furiosus petal dph5 gene and argf gene
9520	22483	35929	2.1	1.1E-01	T72875.1	EST_HUMAN	yt1903.s1 Soares fetal liver spleen INF15 Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:U1181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9546	22509		0.82	1.1E-01	BE68260.1	EST_HUMAN	801438972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
9777	22718		0.89	1.1E-01	BE142305.1	EST_HUMAN	CM3-HT01427108b-026-g11 HT0142 Homo sapiens cDNA
9853	22789		2.05	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-e09 GN0027 Homo sapiens cDNA
10270	23165		0.69	1.1E-01	AL167543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10476	23398		0.45	1.1E-01	BE315509.1	EST_HUMAN	801140231F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3048543 5'
10588	23488		1.01	1.1E-01	R00590.1	EST_HUMAN	y05a09.s1 Soares placenta N24P Homo sapiens cDNA clone IMAGE:147084 3'
10701	23623	37119	1.05	1.1E-01	U60526.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
11156	16103	29017	1.7	1.1E-01	F03265.1	EST_HUMAN	HSC1RE022 normalized infant brain cDNA Homo sapiens cDNA clone c-1r02 3'
11287	24219		3.13	1.1E-01	AF169032.1	NT	Caerulius auratus activin beta A precursor, mRNA, complete cds
11384	24331	37860	3.51	1.1E-01	R23708.1	EST_HUMAN	X43512.r1 Soares placenta N24P Homo sapiens cDNA clone IMAGE:131750 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
11392	24338	37868	1.54	1.1E-01	6981351	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (Pfk), mRNA
11542	24463	38035	2.18	1.1E-01	Z11910.1	NT	Z.mobilis tgi and lig genes encoding RNA guanine transglycosylase and DNA ligase
11542	24463	38036	2.18	1.1E-01	Z11910.1	NT	Z.mobilis tgi and lig genes encoding RNA guanine transglycosylase and DNA ligase
11636	24573	38137	3.68	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12280	25084		2.03	1.1E-01	AA192153.1	EST_HUMAN	393b12.1 Stratiotes muscicola 937209 Homo sapiens cDNA clone IMAGE:627743 5'
12378	25161		3.66	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-0714-03 NT0112 Homo sapiens cDNA
12525	25732		2.18	1.1E-01	BE974596.1	EST_HUMAN	60198051R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
13038	25580		1.89	1.1E-01	BF239753.1	EST_HUMAN	601908350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
13089	25912		1.32	1.1E-01	P14400	SWISSPROT	ELECTROMOTOR NEURON ASSOCIATED PROTEIN 1
1206	14245		2.05	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1277	14312	27273	1.85	1.0E-01	AI695499.1	EST_HUMAN	w60801.x1 NCI_CGAP_K1011 Homo sapiens cDNA clone IMAGE:2495977 3' similar to contains MER7.3
1393	14427	27396	2.25	1.0E-01	AL161504.2	NT	ABYR1 repetitive element
2407	16500	29526	1.16	1.0E-01	AW451365.1	EST_HUMAN	Arabis thaliana DNA chromosome 4, contig fragment No. 16
3524	16570	29493	1.32	1.0E-01	BF033991.1	EST_HUMAN	U14H33-alc-4-07-0-L1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2738420 3'
3732	16774	29686	0.88	1.0E-01	BF239818.1	EST_HUMAN	601456301F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3859849 5'
3849	16889	29792	2.49	1.0E-01	AF297051.1	NT	601908498F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3978	17016	29830	2.66	1.0E-01	BF365703.1	EST_HUMAN	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
4555	17607		0.86	1.0E-01	A172249.1	EST_HUMAN	QV2-NT0048-160800-316-405 NT0048 Homo sapiens cDNA
4657	17672	30863	2.34	1.0E-01	AW952344.1	EST_HUMAN	an32c04.y5 Gascara Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
5287	18274	31138	0.97	1.0E-01	AV721471.1	EST_HUMAN	Drosophila melanogaster tyrosine kinase p45 bcdom (ter) mRNA, complete cds
5273	18279		1.04	1.0E-01	AV763960.1	EST_HUMAN	AV721471 HTB Homo sapiens cDNA clone HTBBQ210 5'
5304	18497		8.1	1.0E-01	W88460.1	EST_HUMAN	AV763960 MDS Homo sapiens cDNA clone MDSBQ311 5'
5492	18592		0.89	1.0E-01	W64015.1	NT	z662h04.s1 Soares fetal_liver_spleen_1NFELS_S1 Homo sapiens cDNA clone IMAGE:116995 3'
5980	18065		0.87	1.0E-01	AK024472.1	NT	Xcampesit genes for sensor and regulator protein
6140	19216	32445	12.15	1.0E-01	AF274875.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6469	19534	32782	0.9	1.0E-01	AA481879.1	EST_HUMAN	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6483	19548	32797	0.95	1.0E-01	AA406039.1	EST_HUMAN	z441910.s1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:766258 3' similar to contains
7220	20242		1.62	1.0E-01	R23821.1	EST_HUMAN	L1.13.1 repetitive element
8008	20947		2.16	1.0E-01	Y12488.1	NT	L1.13.1 repetitive element
8108	21045	34444	0.85	1.0E-01	AJ011400.1	NT	z441910.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:745082 3'
8108	21045	34446	0.85	1.0E-01	AJ011400.1	NT	y344f06.1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:745082 3'
8295	21234	34645	0.63	1.0E-01	AA961091.1	EST_HUMAN	y344f06.1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:745082 3'



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8287	21256	34695	0.45	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8287	21256	34696	0.45	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8505	21474		0.68	1.0E-01	47683365	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8837	21804		0.94	1.0E-01	AW169797.1	EST_HUMAN	x09501.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2675589 3' similar to gp.X17206 40S
9540	22503	35952	1.19	1.0E-01	AF102855.2	NT	Ribosomal protein S4 (RPS4) contains TAR1, a TARI repetitive element
9852	22788	36241	0.54	1.0E-01	R44993.1	EST_HUMAN	Radix norvegicus synaptic SAPAP-interacting protein Synanion mRNA, complete cds
9855	22801		2.05	1.0E-01	M76728.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
9908	22728		2.65	1.0E-01	AE001501.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
9922	22806	36259	0.61	1.0E-01	W01955.1	EST_HUMAN	z09610.s1 Soares, fetal, heart, NH-H19W Homo sapiens cDNA clone IMAGE:327282 3'
10180	23105	36598	1.83	1.0E-01	BF240154.1	EST_HUMAN	601805561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
10295	23220	36703	8.1	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10295	23220	36704	6.1	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10502	23424		0.95	1.0E-01	AW957425.1	EST_HUMAN	EST1368615 MAGE:resequences, MAGE Homo sapiens cDNA
10507	23428	36926	0.55	1.0E-01	T51952.1	EST_HUMAN	y028a06.s1 Strelagene fetal spleen (f867205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
10594	23616	37110	0.89	1.0E-01	BE702750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3930096 5'
11016	23983		1.65	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYROT1 Homo sapiens cDNA clone THYROT100896 3'
11370	24317	37844	2.25	1.0E-01	BF242846.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11370	24317	37845	2.25	1.0E-01	BF242846.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11728	24614	38191	3.16	1.0E-01	BE790543.1	EST_HUMAN	601552556F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
12365	25481		4.11	1.0E-01	BE537719.1	EST_HUMAN	601065564F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12368	25202		2.16	1.0E-01	7682165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12504	25305		2.59	1.0E-01	X00654.1	NT	Drosophila melanogaster fzf gene
12796	25425		1.45	1.0E-01	AA737961.1	EST_HUMAN	px11c06.s1 NCI CGAP_GC3 Homo sapiens cDNA clone IMAGE:1255760 3'
12895	25481		4.47	1.0E-01	BE637719.1	EST_HUMAN	601065564F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12943	25522		1.32	1.0E-01	BE158905.1	EST_HUMAN	CV4-HT001-211295.064-g03 HT0001 Homo sapiens cDNA
12959	25591		6.14	1.0E-01	U66834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
13016	25598		7.59	1.0E-01	AP001507.1	NT	Bacillus thuraciensis genomic DNA, section 1114
2789	15781	28797	1.74	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pkc-RII) mRNA, complete cds
2789	15790	28808	1.71	9.9E-02	BE545564.1	EST_HUMAN	601070210F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2798	15790	28809	1.71	9.9E-02	BE545564.1	EST_HUMAN	601070210F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3280	16334	26254	1.48	9.9E-02	AF068910.1	NT	Homo sapiens neuron III-alpha gene, partial cds

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3974	17014	26628	0.87	9.8E-02	AB21837.1	EST_HUMAN	244563.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740622 3'
4707	17288	30622	1.02	9.8E-02	BE674249.1	EST_HUMAN	7477612.x1 NCL CGAP LU24 Homo sapiens cDNA clone IMAGE:3278988 3'
7044	20086	33373	2.60	9.8E-02	BE613488.1	EST_HUMAN	601504252.F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3906084 5'
7183	18394	31239	7.77	9.8E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds
8247	21216	34624	0.86	9.8E-02	AW103088.1	EST_HUMAN	x445609.x1 NCL CGAP OV23 Homo sapiens cDNA clone IMAGE:2586528 3' similar to contains Alu repetitive element, contains element MIR MIR repetitive element :
8247	21216	34625	0.86	9.8E-02	AW103088.1	EST_HUMAN	x445609.x1 NCL CGAP OV23 Homo sapiens cDNA clone IMAGE:2586528 3' similar to contains Alu repetitive element, contains element MIR MIR repetitive element :
9612	22616	36068	1.23	9.8E-02	6756111	NT	Mus musculus phospholipid transfer protein (Plp), mRNA
9635	13638		1.88	9.8E-02	X56538.1	NT	O. salivaria RAm3y3C gene for alpha-amylose
3160	16216	26130	4.25	9.8E-02	AF184274.1	NT	Daucus carota taucanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4251	17280	30180	6.93	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4251	17280	30181	6.83	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7723	20576		0.84	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9009	22613		1.21	9.8E-02	U61943.1	NT	Human laminin B1 chain gene, exon 28
11788	23843	37465	1.83	9.8E-02	BF037421.1	EST_HUMAN	601480793.F1 NIH_MGC 98 Homo sapiens cDNA clone IMAGE:3864287 5'
12330	25131		1.84	9.8E-02	8383751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1352	14387	27357	1.75	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1589	14821		1.33	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (echinodermoplasm, transmembrane domain) (FGFR3) mRNA
2270	15283	28309	2.78	9.7E-02	BE168660.1	EST_HUMAN	QV1-H1057610/0300-085-404 HT0518 Homo sapiens cDNA
4008	17047		4.89	9.7E-02	Q96795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5418	18521	31398	0.88	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5418	18521	31399	0.88	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6130	19207	32432	1.48	9.7E-02	AW954776.1	EST_HUMAN	EST366548 MAGC resequences, MAGC Homo sapiens cDNA
7517	20482	33843	3.38	9.7E-02	Z989119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2867771 to 3213410
8315	21284	34697	1.09	9.7E-02	N22798.1	EST_HUMAN	W441603.s1 Weizmann Offshoot Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8315	21284	34698	1.09	9.7E-02	N22798.1	EST_HUMAN	W441603.s1 Weizmann Offshoot Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
9201	22167	35597	1.52	9.7E-02	AI953984.1	EST_HUMAN	wx78b06.x1 NCL CGAP OV28 Homo sapiens cDNA clone IMAGE:254788 3'
11529	24470		2.01	9.7E-02	U568337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN); Mus musculus ligandin (Lgn) mRNA, partial cds
2032	15051	28056	1.27	9.8E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1679485 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2032	15051	28067	1.27	9.6E-02	AI080721.1	EST_HUMAN	oz47411.x1 Soares. NIHMPu. S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4372	17399	30279	6.7	9.6E-02	Z33699.2	NT	Proteus mirabilis fibrital operon, strain H4320
5037	18050	30830	1.16	9.6E-02	AW062230.1	EST_HUMAN	EST178303 MAGE ressequencs, MAGI Homo sapiens cDNA
6225	19239		2.63	9.6E-02	BE910039.1	EST_HUMAN	60149808FT NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3800165 5'
8719	21687		0.65	9.6E-02	AU137084.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLACE105740 5'
9902	22954	39315	1.35	9.6E-02	AV687898.1	EST_HUMAN	AV687898 GRC Homo sapiens cDNA clone GKCAH02 5'
10231	23156		1.29	9.6E-02	BE594895.1	EST_HUMAN	601434080FT NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3913363 5'
10398	23321	36805	1.27	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10399	23321	36806	1.27	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10479	23401	36898	0.44	9.6E-02	BF677270.1	EST_HUMAN	60208979FT NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4260969 5'
10511	23433	36930	1.37	9.6E-02	AB013985.1	NT	Anthrithum majus transposon Tarr3 pseudogene for transposase (in S-6 copy)
10511	23433	36931	1.37	9.6E-02	AB013985.1	NT	Anthrithum majus transposon Tarr3 pseudogene for transposase (in S-6 copy)
10621	23943	37043	3.5	9.6E-02	P08174	SWISSPROT	COMPLEMENT DEGRY-ACCELERATING FACTOR PRECURSOR (CD55)
11094	24054	37577	5.31	9.6E-02	Z78702.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
12028	24904	38498	1.53	9.6E-02	AA625755.1	EST_HUMAN	2a81g01.s1 Soares. testis. NIH Homo sapiens cDNA clone IMAGE:745392 3'
12833	25515		1.81	9.6E-02	AI14599.1	EST_HUMAN	ym19h03.s1 Soares. Infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
12895	25553	31719	1.51	9.6E-02	BE728219.1	EST_HUMAN	601563356FT NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3832808 5'
4128	17161	30050	2.66	9.6E-02	AW092395.1	EST_HUMAN	CN2-B100723-060204-087-f12 BN0023 Homo sapiens cDNA
5748	18842	32025	0.51	9.6E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7294	20266	33901	0.51	9.6E-02	AA780728.1	EST_HUMAN	sc68069.s1 Stratagene fetal retina 637202 Homo sapiens cDNA clone IMAGE:387736 3'
7522	20487	33949	4.14	9.6E-02	AB003473.1	NT	Trimeresurus flaviviridis DNA for phospholipase A2 inhibitor, complete cds
7818	20767	34144	7.16	9.6E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7893	18842	32025	0.86	9.6E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
8212	21181	34991	2.95	9.6E-02	BF035961.1	EST_HUMAN	601483942FT NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3857243 5'
8212	21181	34992	2.95	9.6E-02	BF035961.1	EST_HUMAN	601483942FT NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3857243 5'
11039	24003	37529	2.31	9.6E-02	BF035961.1	EST_HUMAN	601483942FT NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3857243 5'
11039	24003	37529	2.31	9.6E-02	BF035961.1	EST_HUMAN	601483942FT NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3857243 5'
1850	14876	27871	4.07	9.4E-02	BF571083.1	EST_HUMAN	60215080FT NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4281917 5'
3894	18634	29844	4.91	9.4E-02	Z33039.1	NT	M. capricornum DNA for CONTIG MC073
5240	19248		0.96	9.4E-02	X08106.1	NT	Lactobacillus bacteriophage phi16 complete genomic DNA
6450	19516	32766	1.21	9.4E-02	AF097363.1	NT	Trichium aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
7651	20767	34173	0.54	9.4E-02	L79833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and pif35 gene, partial cds
8947	21913		2.5	9.4E-02	Z46863.1	NT	Acinetobacter sp. cysD, cysC, cysB, cysA, cysS, rubA, rubB, esbA, esbB, esbC, esbD, esbE, esbF, ppk, mglA, ORF2 and ORF3 genes

Table 4

## Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11280	20797	34173	2.22	9.4E-02	L78533.1	NT	Human BRCA1, Rho7 and cell genes, complete cds, and j435 gene, partial cds
12212	23926		10.73	9.4E-02	U51815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
13087	25617	31692	1.37	9.4E-02	U27659.1	NT	Human pepBGT-1 betaine-GABA transporter mRNA, complete cds
3002	18060		1.71	9.3E-02	4809280	NT	Human sapiens BAI1-associated protein 3 (BAIP3) mRNA
3041	16099		7.39	9.3E-02	6812523	NT	Human sapiens mesenchymal epithelium specific protein 1 (NESG3), mRNA
3270	18324	28247	2.01	9.3E-02	BF575511.1	EST_HUMAN	602133085F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4282259 5'
4179	17210	30096	3.73	9.3E-02	BE391943.1	EST_HUMAN	601286092F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607663 5'
4179	17210	30097	3.73	9.3E-02	BE391943.1	EST_HUMAN	601286092F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607663 5'
4766	17788		2.29	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFALUA06 5'
5745	18839		0.66	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8153	21091	34490	0.59	9.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment H321C010
8591	21559	34975	0.6	9.3E-02	AW566007.1	EST_HUMAN	EST168 Human Fetal Brain MATO-HWAKER cDNA Library Homo sapiens cDNA
9480	22444		0.42	9.3E-02	AL113178.1	NT	Bolety chereza strain T4 cDNA library under conditions of nitrogen deprivation
10068	22995	36484	2.32	9.3E-02	BE962631.2	EST_HUMAN	601655598R1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3855981 3'
10551	23473	36967	3.65	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA032
10551	23473	36968	3.65	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA032
10983	23605		3.59	9.3E-02	AW208117.1	EST_HUMAN	U1H-B11-afkxh-05-0-U1at NCL CGAP_Sub83 Homo sapiens cDNA clone IMAGE:2725553 3'
12482	25750		2.55	9.3E-02	AJ249850.1	NT	Prokaryotic damsel subsp. damselae partial gyb gene for DNA gyrase B subunit
12831	25778		9.12	9.3E-02	AW469350.1	EST_HUMAN	h282812.x1 Soares_NFL_T_GBC_51 Homo sapiens cDNA clone IMAGE:2610837 3'
							Mus musculus major histocompatibility locus class II region, Fc-binding protein Daxx (DAXX) gene, partial cds, Blnq1 (Blnq1), tapasin (tapasin), RelGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr>
13040	26824		2.24	9.3E-02	AF100956.1	NT	Molluscum contagiosum virus subtype 1, complete genome
231	13331	26252	7.81	9.2E-02	U90315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
231	13331	26253	7.81	9.2E-02	U90315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
231	13331	26254	7.81	9.2E-02	U90315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2338	13260		2.72	9.2E-02	R54156.1	EST_HUMAN	y93807.1 Soares infant brain 1M1B Homo sapiens cDNA clone IMAGE:41618 5'
3194	16249	28167	3.72	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3316	16369	28259	0.99	9.2E-02	AA534354.1	EST_HUMAN	nt79601.1 NC_001 CGAP_C03 Homo sapiens cDNA clone IMAGE:326136 3'
3559	16544		1.27	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
4266	17295		1.24	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, late/cy-associated transcript, promoter region
4337	17364		0.84	9.2E-02	BE289722.1	EST_HUMAN	600844365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2660176 5'
4666	17689	30575	1.4	9.2E-02	X96402.1	NT	G.gallus Virus-CK gene
8842	21311	34725	1.87	9.2E-02	T46920.1	EST_HUMAN	y698c09.1 Stralagene placenta (#637225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb-X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8517	21485	34899	2.19	9.2E-02	X95256.1	NT	H. vulgare xylose isomerase gene
12002	24879	38475	1.74	9.2E-02	AF026552.3	NT	Mesocricetus auratus oviduct precursor (OVI) gene, complete cds
13019	25986		1.31	9.2E-02	11466872	NT	Podocarpa artemia mitochondrion, complete genome
423	13118	28017	7.92	9.1E-02	X77655.1	NT	O. cuticularis k12 keratin gene
3684	16727		0.96	9.1E-02	AF372569.1	EST_HUMAN	PM2-BT0349-161299-201-102 BT0349 Homo sapiens cDNA
4510	17635	30419	1.5	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5304	18307		0.98	9.1E-02	AB010868.1	NT	Clona infestialis endostyle-specific mRNA, complete cds
5819	18609	32093	1.27	9.1E-02	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, Gbb, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7528	26000		0.52	9.1E-02	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
7615	20576	33939	12.92	9.1E-02	AW160658.1	EST_HUMAN	aut4a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781969.5
7937	20879	34269	0.74	9.1E-02	AF000061.1	NT	Aeropyrum pernix genomic DNA, section 4/7
7977	20616	34307	0.87	9.1E-02	U39073.1	NT	Mus musculus thymopollin zeta mRNA, complete cds
9276	22242	35671	0.95	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10763	23714		1.84	9.1E-02	T02694.1	EST_HUMAN	FB19710 Fetal brain, Strategene Homo sapiens cDNA clone FB19710.3 end
10823	23744	37245	1.24	9.1E-02	S74059.1	NT	Tg616-Cy1 actin [Tripneustes gratilla=sea urchins, embryos, Genomic, 8276 nt]
10852	23772	37271	0.8	9.1E-02	Y11187.1	NT	A.thaliana RH1, TC1, G14897-S, G14897-6, and PRL1 genes
12151	25009		3.53	9.1E-02	5633494	NT	Bacteriophage M1, complete genome
12993	25919		2.15	9.1E-02	AA179901.1	EST_HUMAN	339H12.s1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:611783.3 similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12468	25217		1.82	9.1E-02	AF052865.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
12915	25771		1.78	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
							FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOY16) (KB CELLS FBP)
746	13907	26747	6.38	9.0E-02	P15328	SWISSPROT	ANTIGEN MOY16 (KB CELLS FBP)
							h339g10.x1 NCI_CGAP_Lu21 Homo sapiens cDNA clone IMAGE:3775942.3 similar to contains Alu repetitive element
1640	14672	27645	6.7	9.0E-02	BE20482.1	EST_HUMAN	HIV-1 p8095-06 from USA envelope glycoprotein (env) gene, partial cds
2815	15907	28826	6.5	9.0E-02	AF135522.1	NT	HIV-1 p8095-06 from USA envelope glycoprotein (env) gene, partial cds
2815	15907	28827	6.5	9.0E-02	AF135522.1	NT	HIV-1 p8095-06 from USA envelope glycoprotein (env) gene, partial cds
3347	15998	29321	1.11	9.0E-02	AF1279135.1	NT	Dicystidium discoidum spore coat structural protein SP65 (coE) gene, complete cds
4328	17566	30243	0.83	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Salmon sciurus=squirrel monkeys, liver, mRNA, 1474 nt]
4328	17566	30244	0.83	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Salmon sciurus=squirrel monkeys, liver, mRNA, 1474 nt]

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Table 4

### Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4448	17474	30393	1.25	9.0E-02	P95268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ)
4695	17716	30611	2.37	9.0E-02	Q95740.2	NT	Pleurocidium falciparum P-type ATPase 3 gene
5291	18289	31137	0.93	9.0E-02	Q24597	SWISSPROT	REGULATORY PROTEIN ZESTIE
6110	19189	32409	14.12	9.0E-02	W59037.1	EST_HUMAN	zsf88.12.r1 Scarsa_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:297894 3' similar to PRK582171 S52171 small G protein - human 1
6680	19932		1.14	9.0E-02	BF062951.1	EST_HUMAN	7h63803.x1 NCI_CGAP_Go618 Homo sapiens cDNA clone IMAGE:3320845 3' similar to contains ALU repetitive element;
6931	20155	33473	0.88	9.0E-02	R82905.1	EST_HUMAN	X111508.x1 Scarsa_placenta_N241P Homo sapiens cDNA clone IMAGE:139903 3'
12762	25404		2.03	9.0E-02	AF02236.1	NT	Escherichia coli strain E2348/89 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EacR (eacR), EacS (eacS), EacT (eacT), EacU (eacU), Csd (cscD), EecC (eacC), EecJ (eacJ), SepZ (sepZ), EacV (eacV), EacN (eacN), SepQ (sepQ), Ttr (ttr), OrfU (orfU), >
1432	14466	27442	2.04	8.9E-02	BF701593.1	EST_HUMAN	60212003072.NH_MGC_58 Homo sapiens cDNA clone IMAGE:4285931 5'
1432	14468	27443	2.04	8.9E-02	BF701593.1	EST_HUMAN	60212003072.NH_MGC_58 Homo sapiens cDNA clone IMAGE:4285931 5'
2398	15403	28429	1.1	8.9E-02	BE153572.1	EST_HUMAN	PM0170339.251169-003-401 HT0339 Homo sapiens cDNA
4227	17258		2	8.9E-02	AF290655.1	NT	Atchicum argusatum AtranFic2 protein (AtranFic2) gene, partial cds
5960	19036	32230	2.64	8.9E-02	AW452122.1	EST_HUMAN	U1-HB3-als-048-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5960	19038	32231	2.64	8.9E-02	AW452122.1	EST_HUMAN	U1-HB3-als-048-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5968	19051	32252	3.5	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC68107), mRNA
7399	20397	33720	1.49	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETHETRAHYDROFOLATE DEHYDROGENASE ; METHYLENETHETRAHYDROFOLATE CYCLOHYDROLASE]
7507	20757		2.02	8.9E-02	Z79021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SCSpA20FB
8985	21354	34762	0.77	8.9E-02	P28475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (GNOS)
8468	21437	34855	0.7	8.9E-02	BF701965.1	EST_HUMAN	602129111F2.NH_MGC_58 Homo sapiens cDNA clone IMAGE:4285827 5'
8468	21437	34856	0.7	8.9E-02	BF701965.1	EST_HUMAN	602129111F2.NH_MGC_58 Homo sapiens cDNA clone IMAGE:4285827 5'
8945	21911	35336	5.01	8.9E-02	AA300319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9978	22905	36389	0.62	8.9E-02	AI295927.1	EST_HUMAN	qu55605.x1 NCI_CGAP_Lym18 Homo sapiens cDNA clone IMAGE:1969680 3' similar to contains MER10.b1 MER10 repetitive element ;
9978	22905	36370	0.62	8.9E-02	AI295927.1	EST_HUMAN	qu55605.x1 NCI_CGAP_Lym18 Homo sapiens cDNA clone IMAGE:1969680 3' similar to contains MER10.b1 MER10 repetitive element ;
10090	23016	39492	0.87	8.9E-02	AA339358.1	EST_HUMAN	EST44454 Fetal brain 1 Homo sapiens cDNA 5' end
12159	25743		1.3	8.9E-02	P30143	SWISSPROT	HYPOTHETICAL 61.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
12211	25754		1.91	8.9E-02	P16824	SWISSPROT	MYOSIN-2 ISOFORM
25176	25176		9.08	8.9E-02	BE85918.1	EST_HUMAN	6021296823.NH_MGC_58 Homo sapiens cDNA clone IMAGE:4293180 5'
72367	25164		9.08	8.9E-02	BE85918.1	EST_HUMAN	6021296823.NH_MGC_58 Homo sapiens cDNA clone IMAGE:4293180 5'

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12530	25258		1.81	8.9E-02	6680220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA
12571	25282		1.5	8.5E-02	U29895.1	NT	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
1374	14408	27378	1.26	8.8E-02	Q27474	SWISSPROT	Probable DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))
3921	16861	28874	1.03	8.8E-02	A4289128.1	EST_HUMAN	EST11656 Uleus Homo sapiens cDNA, 5' end
4065	17101		3.7	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TF1D 135 KDA SUBUNIT (TAF1135) (TAF1130) (TAF1130)
4267	17296		1.26	8.8E-02	4602804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4331	17359		2.3	8.8E-02	4680423	NT	Homo sapiens paired box gene 6 (emilia, keratins) (PAX6), isoform b, mRNA
7782	20744		0.86	8.8E-02	D17520.1	NT	Sheep mRNA for angiotensinogen, complete cds
6939	22304	35732	1.32	8.8E-02	AA151872.1	EST_HUMAN	zr6a05.s1 Strategic clone (f837204) Homo sapiens cDNA clone IMAGE:566288 3'
11453	24396	37941	3.43	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3839648 5'
11453	24396	37942	3.43	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3839648 5'
11563	24531	38038	5.78	8.8E-02	AL040129.1	EST_HUMAN	DKFZ434D1313.11.434 (synonym: bias3) Homo sapiens cDNA clone DKFZ434D1313 5'
12441	25204	31827	2.4	8.8E-02	Z71661.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL285w
1854	14866	27661	1.55	8.7E-02	AI167281.1	EST_HUMAN	ox65b01.s1 Scores, NihMPC, S1 Homo sapiens cDNA clone IMAGE:1661161 3'
3707	16750	29665	3.84	8.7E-02	U82965.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3707	16750	29666	3.84	8.7E-02	U82965.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4736	17756	30650	1.2	8.7E-02	AF176636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5138	18147		1.02	8.7E-02	AE000985.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5166	18175	31053	0.97	8.7E-02	6863384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
5367	18490	31366	6.04	8.7E-02	AA286875.1	EST_HUMAN	zsa55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5367	18490	31366	6.04	8.7E-02	AA286875.1	EST_HUMAN	zsa55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
7022	20147	33466	0.81	8.7E-02	AL271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7022	20147	33467	0.81	8.7E-02	AL271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7243	19878	33275	0.83	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TA1-binding protein 1 mRNA, partial cds
8860	21827	35250	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
8860	21827	35251	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
11057	24930		2.15	8.7E-02	U04758.1	NT	Oryctolagus cuniculus cyclochrome P-450 (CYP4A4) gene, 5' end
11641	24578	38144	1.79	8.7E-02	AL007783.1	NT	Glucobacter oxydans RNA-III and RNA-IIIa genes





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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8853	21918	35345	1.92	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
10196	23121	39607	3.17	8.5E-02	BE833054.1	EST_HUMAN	RC4-O10037-200700-014-05 OT0037 Homo sapiens cDNA
10196	23121	39608	3.17	8.5E-02	BE833054.1	EST_HUMAN	RC4-O10037-200700-014-05 OT0037 Homo sapiens cDNA
10338	23382	38742	0.44	8.5E-02	AI140618.1	EST_HUMAN	qel0505.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:738136 3'
10729	23850	37143	0.56	8.5E-02	TG76731.1	NT	V.ammodontes gene for ammodontin C
10851	23771	37270	1	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11460	24433	37989	8.1	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11507	24448	37989	4.05	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12985	25547	38557	5.18	8.5E-02	AA362634.1	EST_HUMAN	EST172736 Ovary II Homo sapiens cDNA 5' end
2675	15901	28690	3.99	8.4E-02	W69330.1	EST_HUMAN	z04411.t1 Soares, fetal heart_NBHH19W Homo sapiens cDNA clone IMAGE:343632 5'
4381	17409	30290	1.02	8.4E-02	AF257213.1	NT	Gavia pacellus glycoprotein alpha-subunit mRNA, complete cds
4381	17409	30291	1.02	8.4E-02	AF257213.1	NT	Gavia pacellus glycoprotein alpha-subunit mRNA, complete cds
5235	18243	31115	0.98	8.4E-02	5453817	NT	Homo sapiens nucleobindin 1 (NUCB1), mRNA
5385	18488	31363	8.74	8.4E-02	BE267153.1	EST_HUMAN	6071604561.NIH.JMGC.7 Homo sapiens cDNA clone IMAGE:3534583 5'
6947	19900	33194	1.86	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
8363	21332	34744	7.84	8.4E-02	BE096074.1	EST_HUMAN	CM9-B10790-260400-162-d05 B10790 Homo sapiens cDNA
9194	22160	35538	1.02	8.4E-02	AF218990.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2
10727	23849	37142	1.9	8.4E-02	AI735184.1	EST_HUMAN	as89g10.x1 Borestead colon HPLR37 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:088312
12851	25146	31853	1.46	8.4E-02	R79408.1	EST_HUMAN	088312 GDB-4.1
2027	15047	28090	0.97	8.3E-02	5935680	NT	YB3H12.11 Scores Plectra N22HP Homo sapiens cDNA clone IMAGE:145855 5'
2027	15047	28091	0.97	8.3E-02	5935680	NT	YB3H12.11 Scores Plectra N22HP Homo sapiens cDNA clone IMAGE:145855 5'
3603	16551	29568	0.61	8.3E-02	TG75334	SW/ISSPROT	Ixodes hexagonus mitochondrion, complete genome
3634	16677	29569	0.68	8.3E-02	AI436797.1	EST_HUMAN	HYPOHEMICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3634	16677	29569	0.68	8.3E-02	AI436797.1	EST_HUMAN	th2g06.x1 Soares, NIHMP.u, S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6393	19457	32702	0.78	8.3E-02	AI942338.1	EST_HUMAN	th2g06.x1 Soares, NIHMP.u, S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6502	19566	32818	2.54	8.3E-02	AF052983.1	NT	w078f11.x1 NC1 CGAP Kid1 Homo sapiens cDNA clone IMAGE:2461581 3'
8513	21282	34694	3.61	8.3E-02	AF196787.1	NT	Homo sapiens proteolipin 43 gene, exon 1
8513	21282	34694	3.61	8.3E-02	AF196787.1	NT	Rattus norvegicus desphosphin-related protein 2 A-form splice variant (Dmp2) mRNA, complete cds
8546	21315	34694	1.19	8.3E-02	AA965285.1	EST_HUMAN	cg89g08.x1 NC1 CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1, L1 L1 L1
8842	21610	34694	1.54	8.3E-02	AA987873.1	EST_HUMAN	cg89h10.x1 NC1 CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1502779 3'
9896	22849	36306	1.58	8.3E-02	AW583503.1	EST_HUMAN	cg89h10.x1 Homo Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
9909	22730	36306	2.19	8.3E-02	AL161595.2	NT	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE ; Arabidopsis thaliana DNA chromosome 4, coding fragment No. 91

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10706	23828		0.5	8.3E-02	AF020409.1	NT	Dichotylidium discoidium DocA (docA) mRNA, complete cds
12444	25924		1.48	8.3E-02	BE989458.1	EST_HUMAN	B0164770F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3926983 5'
1379	14413		7.44	8.2E-02	Y06170.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
1494	14521	27498	1.77	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3089	1847		2.24	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3815	16855		1.61	8.2E-02	AL161438.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4033	17071	28972	1.22	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4313	17342	30222	5.83	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4313	17342	30223	5.83	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4313	17342	30224	5.83	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5108	18118	30962	1.29	8.2E-02	AF240778.1	NT	Mus musculus pepsinogen F (PepF) mRNA, complete cds
5118	18128	31004	4.13	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5300	18128	31004	0.95	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5408	18511	31389	1.47	8.2E-02	BE897030.1	EST_HUMAN	G01439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
7221	20243	33577	2.84	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
9005	20944		0.6	8.2E-02	AF743341.1	EST_HUMAN	A7743341 CB Homo sapiens cDNA clone CBLAN507 5'
9057	22023		0.46	8.2E-02	U26987.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
9124	22090	35518	2.75	8.2E-02	AW875126.1	EST_HUMAN	BC02-PT0004-031299-011-403 PT0004 Homo sapiens cDNA
8958	22885	36346	5.43	8.2E-02	X04197.1	NT	Best necrotic yellow vein virus RNA-2
10121	22047	36526	2.38	8.2E-02	BE264318.1	EST_HUMAN	G01115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355598 5'
12450	25208	31631	6.88	8.2E-02	AE002468.2	NT	Chlamydia pneumoniae A339, section 73 of 94 of the complete genome
12835	25710		5.74	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1483	14626	27498	1.05	8.1E-02	AB017138.1	NT	Pseudomonas putida melonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcF, mdcG, mdcH, mdcI, and mdcM genes), complete cds
5948	18938	32123	1.05	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6516	19679	32836	1.38	8.1E-02	T11632.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7403	20371		0.81	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7335	20782		0.9	8.1E-02	AI692681.1	EST_HUMAN	wb85698.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8683	21651	35072	0.53	8.1E-02	11428974	NT	Homo sapiens hypothetical protein FL10060 (FL10060) mRNA
8683	21651	35073	0.53	8.1E-02	11428974	NT	Homo sapiens hypothetical protein FL10060 (FL10060) mRNA
10272	23187		1.58	8.1E-02	AY005160.1	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
11877	24710	38294	1.53	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	15930	28026	4.82	8.0E-02	AW964653.1	EST_HUMAN	EST385723 MAGIE resequences, MAGC Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1709	15875	27722	13.63	8.0E-02	D28555.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1709	15875	27722	13.63	8.0E-02	D28555.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1819	14843	27939	4.07	8.0E-02	BE067219.1	EST_HUMAN	PM3-3T0347-17020-001-508 BT0347 Homo sapiens cDNA
2384	15382	28417	1.05	8.0E-02	D90915.1	NT	Synochocytis sp. PCC8803 complete genome, 17/27, 2137259-2267269
2384	15382	28418	1.05	8.0E-02	D90915.1	NT	Synochocytis sp. PCC8803 complete genome, 17/27, 2137259-2267269
2478	15482	28418	4.69	8.0E-02	BF246744.1	EST_HUMAN	60185548F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4075619 5'
2831	14137	27088	0.99	8.0E-02	M23449.1	NT	Diclyadema discoidum cyclic nucleotide phosphodiesterase gene, complete cds
2911	15869	28692	0.76	8.0E-02	AL445087.1	NT	Thermoplasma acidophilum complete genomes, segment 5/5
3830	16870	29772	8.64	8.0E-02	AW366118.1	EST_HUMAN	EST1378191 MAGE resequences, MAGE Homo sapiens cDNA
4810	17927	30724	1.7	8.0E-02	AL434202.1	EST_HUMAN	EST1922.1 NCI_CGAP_Gae4 Homo sapiens cDNA clone IMAGE:2132114 3'
4818	17835	30733	0.89	8.0E-02	AF116596.1	NT	Arabidopsis thaliana putative transcription factor (HUA2) mRNA, complete cds
4852	17869	30733	7.57	8.0E-02	X72794.1	NT	Musculus gene for gelatinase B
5832	18822	32105	0.71	8.0E-02	AW651139.1	EST_HUMAN	EST383209 MAGE resequences, MAGE Homo sapiens cDNA
5993	19077	32274	3.28	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7386	19077	32274	1.44	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8465	21434	34851	3.74	8.0E-02	AL14693.1	NT	Bordetella pertussis strain 14 cDNA library under conditions of nitrogen deprivation
9744	22685	36139	1.21	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9744	22685	36140	1.21	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10519	23441		0.6	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
11145	24105	37632	2.16	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M89, and ADP-ribosylation factor related protein 1 (ARHNP1) genes, complete cds
12483	25230	31768	6.54	8.0E-02	AJ005375.1	NT	Drosophila arena hunchback region
13306	18942		2.06	8.0E-02	4593034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2184	15199	28219	4.36	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959610 5'
2892	16050	28971	8.43	7.9E-02	AI562029.1	EST_HUMAN	ar9ec08.x1 Bartshead colon HPL-8B7 Homo sapiens cDNA clone IMAGE:2173846 3' similar to gb:Z8878
3864	16903	29808	5.68	7.9E-02	6681044	NT	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3864	16903	29809	5.68	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
4722	17442	30633	1.08	7.9E-02	BF348454.1	EST_HUMAN	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
4849	17869		1.49	7.9E-02	AB008019.1	NT	60201870F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4155401 5'
6955	19008		1.06	7.9E-02	BF368016.1	EST_HUMAN	ARAD03 thalassaemia RXX424L mRNA, partial cds
8366	21335	34747	3.26	7.9E-02	U27832.1	NT	RC3-ON042-31080-024-4T1 GN0042 Homo sapiens cDNA
10388	23310	36788	4.89	7.9E-02	AI081544.1	EST_HUMAN	Saccharomyces cerevisiae suppressor of Mif2 Smk4p (SM14) gene, complete cds
							ou63805 at NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP-C37A2.2
							CE08811;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10388	23310	35789	4.89	7.8E-02	A081644.1	EST_HUMAN	063005.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1832465 3' similar to WP_C37A2.2 CE08811:
1215	14253	27210	1.69	7.8E-02	A1769376.1	EST_HUMAN	065802.y6 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1670487 5' similar to contains L1.13 L1 repetitive element;
1215	14253	27211	1.69	7.8E-02	A1769376.1	EST_HUMAN	065802.y6 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1670487 5' similar to contains L1.13 L1 repetitive element;
5123	18804		3.25	7.8E-02	BE260048.1	EST_HUMAN	600943055:1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2968893 5'
7279	20013	33317	1.29	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; end plasmid membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7279	20013	33318	1.29	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; end plasmid membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
9137	22103	35528	1.28	7.8E-02	BE897947.1	EST_HUMAN	601440439:1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
8232	22188	35626	0.6	7.8E-02	X78344.1	NT	S.cerevisiae CAT8 gene
9408	22373	35808	0.66	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9408	22373	35809	0.66	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9716	22744	36195	1.23	7.8E-02	AA469354.1	EST_HUMAN	nc88b06.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:771731
10161	23086	36593	0.65	7.8E-02	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21), from 3869281 to 4214814
12114	24084	35685	1.64	7.8E-02	BF025981.1	EST_HUMAN	60166597BF1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3953083 5'
1389	18887	27402	0.93	7.7E-02	AF181887.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3000	18845		2.06	7.7E-02	AJ296953.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5622	18718	31877	0.61	7.7E-02	AF062638.1	NT	Gallus gallus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds
8241	21210	34615	7.34	7.7E-02	AA402948.1	EST_HUMAN	zr33d1.1.1 Soares ovary tumor NihOT Homo sapiens cDNA clone IMAGE:741717 5' similar to
10195	23120	35605	3.76	7.7E-02	P38080	SWISSPROT	TR.G1173905 G1173905 SPICEOSOME ASSOCIATED PROTEIN ; PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10490	23412	35609	0.78	7.7E-02	A1318692.1	EST_HUMAN	1680608.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:226876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10490	23412	35910	0.76	7.7E-02	A1318692.1	EST_HUMAN	1680608.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:226876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
11352	24302	37829	4.65	7.7E-02		NT	Homo sapiens KIA00628 gene product (KIA00628), mRNA
12671	25785		1.91	7.7E-02	11436859	NT	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3398	1847	29373	2.43	7.8E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634503 5'
3419	18467	29387	1	7.8E-02	AA396447.1	EST_HUMAN	EST117214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to proteasheir 43
6216	19290	32523	0.72	7.8E-02	AB01275.1	EST_HUMAN	an2502.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'
6491	19556	32806	0.87	7.8E-02	BE379328.1	EST_HUMAN	601239402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9725	22753	36206	1.35	7.8E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
10257	23182		1.42	7.8E-02	AL190782.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/8
10980	23602	36994	0.47	7.8E-02	BE1798002.1	EST_HUMAN	RC4-H10546-020900-017-008 RT0546 Homo sapiens cDNA
10714	23636		0.56	7.8E-02	BE959639.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10952	23872	37384	0.67	7.8E-02	X82656.1	NT	L. esculentum mRNA for those phosphatase translocator
10952	23872	37385	0.67	7.8E-02	X82656.1	NT	L. esculentum mRNA for those phosphatase translocator
11998	24893	39459	1.9	7.8E-02	AW996645.1	EST_HUMAN	QV3-BN0046-150400-151-004 BN0046 Homo sapiens cDNA
785	13645	26790	2.99	7.8E-02	5902063	NT	Homo sapiens cdule carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
785	13645	26791	2.89	7.8E-02	5902063	NT	Homo sapiens cdule carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1935	14959	27965	0.93	7.5E-02	AL183278.2	NT	Homo sapiens echulose 21 segment HS21C078
4536	17559	30447	0.63	7.8E-02	AB015661.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
5952	19037	32233	0.71	7.5E-02	AI948714.1	EST_HUMAN	wg2408.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
8681	21649	35071	1.01	7.5E-02	AI864367.1	EST_HUMAN	w52002.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428481 3' similar to gb:MI4328 ALPHA
8852	21819	35259	1.29	7.5E-02	AUT16913.1	EST_HUMAN	ENCLOSE (HUMAN);
10392	23314		0.45	7.5E-02	BF221730.1	EST_HUMAN	AUT16913 HEMBA1 Homo sapiens cDNA clone HEMBA100284 5'
10859	23779	37279	0.9	7.5E-02	BF206909.1	EST_HUMAN	7061005.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
10953	23873	37366	0.66	7.4E-02	X79460.1	NT	MER27 repetitive element ;
4758	13450	29478	1.24	7.4E-02	AW838547.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
1456	14489		1.08	7.4E-02	AF030027.1	NT	G.fiml DSM 20113 16S rDNA
2965	15586		0.99	7.4E-02	6755069	NT	RC5L T0054-260100-011-H08 LT0054 Homo sapiens cDNA
3309	16653	29571	0.78	7.4E-02	AI807885.1	EST_HUMAN	Equine herpesvirus 4 strain NS80567, complete genome
4733	17783	30646	1.09	7.4E-02	L78810.1	NT	wf4301.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356365 3'
4833	17850	30750	3.24	7.4E-02		NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4879	17994	30883	2.52	7.4E-02	6678442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl), mRNA
6643	19701		1.8	7.4E-02	R17477.1	EST_HUMAN	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchlp), mRNA
7707	20664	34031	0.78	7.4E-02	AA605132.1	EST_HUMAN	X914606.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
							ne71d02.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1172259 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8233	21202	34608	1.2	7.4E-02	BE80112.1	EST_HUMAN	601463306F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895204.5'
8846	21813	35233	1.01	7.4E-02	U56089.1	NT	Human perlecan hyaluronan protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9521	22484	35630	1.02	7.4E-02	AW629605.1	EST_HUMAN	ih67d11.y1 NCL CGAP_GUT Homo sapiens cDNA clone IMAGE:2867861.5' similar to SW_SCA2_HUMAN
9521	22484	35931	1.02	7.4E-02	AW629605.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.1
9764	21117	34516	0.48	7.4E-02	AI672539.1	EST_HUMAN	ih67d11.y1 NCL CGAP_GUT Homo sapiens cDNA clone IMAGE:2867861.5' similar to SW_SCA2_HUMAN
9764	21117	34517	0.48	7.4E-02	AI672539.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.1
10173	23098	36578	1.07	7.4E-02	U62293.1	EST_HUMAN	we74d02.x1 Soares_Dickgraefe colon_NHCD Homo sapiens cDNA clone IMAGE:2346819.3'
10301	23226	36708	0.53	7.4E-02	BF512678.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
12408	25181		1.47	7.4E-02	11525993	NT	UII-H-BW1-ang-q-08-Q-UI.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3068998.3'
12665	25503		2.51	7.4E-02	AW379431.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
469	13542	26468	1.3	7.3E-02	BE564961.2	EST_HUMAN	GM44HT0243-081106-037-d11 HT0243 Homo sapiens cDNA
489	13542	26469	1.3	7.3E-02	BE564961.2	EST_HUMAN	601658758R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209.3'
985	13748	26674	5.48	7.3E-02	AE001789.1	NT	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209.3'
1477	15669	27486	3.94	7.3E-02	AW900291.1	EST_HUMAN	Thermatoga maritima section 10T of 136 of the complete genome
1862	15679		15.78	7.3E-02	AL163302.2	NT	GM0-NN1004-130300-294-g08 NN1004 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C102
							Human geminin T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCBBV2/751P, TCBBV2251A2N1T, TCBBV651A1T, TCBBV751A1N2T, TCBBV551A1T, TCBBV133S, TCBBV65TP, TCBBV753A2T, TCBBV133A21T, TCBBV652A2P1T, TCBBV752A1N4T, TCBBV133S9/133>
3785	18626		0.72	7.3E-02	U66059.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
5032	18046		1.06	7.3E-02	U12283.1	NT	
6595	19655	32927	1.04	7.3E-02	AA778977.1	EST_HUMAN	g24d02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451176.3' similar to gbl02d426.26S PROTEASE SUBUNIT 4 (HUMAN);
7708	20683	34029	2.47	7.3E-02	P05143	SWISSPROT	
7706	20683	34030	2.47	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8508	21476		1.2	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
9565	22527		1.39	7.3E-02	AB011090.1	NT	Homo sapiens mRNA for KIAA0519 protein, partial cds
11552	19655	32927	1.89	7.3E-02	AA778977.1	EST_HUMAN	g24d02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451176.3' similar to gbl02d426.26S PROTEASE SUBUNIT 4 (HUMAN);
12925	25510		1.33	7.3E-02	Z73367.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241C
							Methanobacterium thermoautotrophicum from bases 1028155 to 1038934 (section 88 of 148) of the complete genome
120	13229	26156	0.7	7.2E-02	AE000882.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
120	13229	26157	0.7	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1472	14505	27478	2.71	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1472	14505	27479	2.71	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2558	15558		2.88	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
3900	16940	29851	0.74	7.2E-02	AW298322.1	EST_HUMAN	U1H-BW70-q1a-05-Q-U1st1 NCI CGAP SubB Homo sapiens cDNA clone IMAGE:2732049 3'
4373	17400	30280	4.87	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4251950 5'
5360	18465	31336	2.81	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5361	18466	31337	8.14	7.2E-02	P11120	SWISSPROT	CALMODULIN
6239	18312		0.73	7.2E-02	BF217596.1	EST_HUMAN	601863905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4058224 5'
7374	20344	33686	1.78	7.2E-02	BF216086.1	EST_HUMAN	601883559F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4059710 5'
7391	20380	33712	0.6	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7417	20384		1.74	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative histidine kinase (zmpS), complete genome
8529	21497	34912	0.88	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8529	21497	34913	0.88	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
9419	22394		0.92	7.2E-02	Y17217.1	NT	Lactococcus lactis cept gene
9934	22861		0.83	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9970	22937	36360	1.88	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAUG01 5'
10117	23043	36523	3.83	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10274	23189	36883	1.17	7.2E-02	BF125399.1	EST_HUMAN	6017683523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026438 5'
10362	23285	36762	2.26	7.2E-02	AW873187.1	EST_HUMAN	h24f11.x1 NCI CGAP Ad1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR.Q823.40 Q82340
10552	23474	36806	0.84	7.2E-02	AA768204.1	EST_HUMAN	ca62207.s1 NCI CGAP_G031 Homo sapiens cDNA clone IMAGE:1316844 3'
10717	23639	37132	2.17	7.2E-02	U82685.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28TS protein (XQ28ORF), and blycyan (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10840	23760	37260	5.41	7.2E-02	BE565003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3985591 5'
10864	23764		3.24	7.2E-02	BE50214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451550 5'
11298	24210	37733	4.17	7.2E-02	AF049874.1	NT	Rattus norvegicus BHLH transcription factor Miert1 (Miert) gene, complete cds
12311	25119	31842	1.88	7.2E-02	AA773686.1	EST_HUMAN	ad1a04.1r Soares, NHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12350	25145		5.13	7.2E-02	AJ230786.1	EST_HUMAN	AJ230786 Homo sapiens library (Seranidi P) Homo sapiens cDNA clone PS13D53

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Exposition Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12469	25218		3.89	7.2E-02	U63838.1	NT	Homo sapiens elaxia telangiectasia (ATM) gene, complete cds
12469	25218		8.41	7.2E-02	AW900962.1	EST_HUMAN	CMANNN1009-200300-110-c11 NN1009 Homo sapiens cDNA
12880	25533		1.45	7.2E-02	AF020439.1	NT	Homo sapiens A TP-citrate lyase gene, Intron 3
12964	25533		1.85	7.2E-02	AA401779.1	EST_HUMAN	z5f7c12.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:726454 5'
1820	14944	27640	1.83	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2300	18512	26332	6.39	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092881 5'
8236	21208	34612	0.87	7.1E-02	A125284.1	EST_HUMAN	q692a10.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1736922 3'
12183	25038		8.33	7.1E-02	BE304784.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
529	13600	26518	1.42	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1498	14532		1.82	7.0E-02	X96577.1	NT	Martellia Mleu1-1 gene
1778	14805	27191	1.18	7.0E-02	AJ005943.1	EST_HUMAN	Z68004.s1 Strategene colon (#937204) Homo sapiens cDNA clone IMAGE:509598 3'
3042	18100	29015	1.76	7.0E-02	AW138192.1	EST_HUMAN	U1-H-B1-acy-c-07-Q-U1 s1 NC1 CGAP SUB3 Homo sapiens cDNA clone IMAGE:2716020 3'
3913	19553	29894	0.96	7.0E-02	AA815438.1	EST_HUMAN	a165a12.s1 Soares, testis, NHT Homo sapiens cDNA clone 1375878 3' similar to gb:K03002 80S
4074	17110	30004	1.05	7.0E-02	BE070264.1	EST_HUMAN	QVABT0407-280100-09D-s10 BT0407 Homo sapiens cDNA
4164	17185		1.24	7.0E-02	AW762662.1	EST_HUMAN	CMO-JM0001-080300-270-s12 UN0001 Homo sapiens cDNA
4242	17271	30156	1.28	7.0E-02	AF071921.1	NT	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
4866	17981	30871	8.41	7.0E-02	BF361987.1	EST_HUMAN	601181629F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4050071 5'
5457	18553		1.03	7.0E-02	Y09143.2	NT	Lumbricus rubellus mRNA for cyclophilin B
7630	20590	33953	0.9	7.0E-02	AV680285.1	EST_HUMAN	AV680285 GK Homo sapiens cDNA clone GKCAE08 5'
7894	20088	34186	0.8	7.0E-02	Y19187.1	NT	Gallus gallus mRNA for partial acotin, XL spliced variant (acc gene)
8454	22418	35856	1.2	7.0E-02	9628113	NT	African swine fever virus, complete genome
9556	22883	35345	1.21	7.0E-02	K02901.1	NT	Rat Ig gamma epsilon H-chain gene C-region, 3' end
10312	23236	35718	0.76	7.0E-02	U27266.1	NT	Human myosin binding protein H (MYBP-H) gene, complete cds
11700	24685	38242	2.23	7.0E-02	AA724265.1	EST_HUMAN	ah96a05.s1 Soares, NFL, LOC_51 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837
12639	25519	31710	1.68	7.0E-02	11421633	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
515	13586	26504	11.2	6.9E-02	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
515	13586	26505	11.2	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
515	13586	26505	11.2	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1396	14370		1.68	6.9E-02	4507968	NT	Homo sapiens regulator of Gs-selective protein signalling (ZGAP1) mRNA, and translated products
3807	18847	29754	1.37	6.9E-02	Q06364	SWISSPROT	28S PROTEASOME REGULATORY SUBUNIT S2 (NUCLEAR ANTIGEN 21D7)
3807	18847	29755	1.37	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)



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5151	18161	31041	0.97	6.9E-02	AA670289.1	EST_HUMAN	at259a08.s1 Soares, total, fetus, N2H-F8_gw Homo sapiens cDNA clone IMAGE:1032710 3'
6026	19109		0.57	6.9E-02	AF161954.1	NT	Homo sapiens HSPC101 mRNA, partial cds
7876	20820		0.67	6.9E-02	AF164967.1	NT	Ganine distemper virus strain A75/17, complete genome
8387	21356		1.18	6.9E-02	U12022.1	NT	Human calmodulin (CALMT) gene, exons 2,3,4,5 and 6, and complete cds
8699	21865	35287	1.08	6.9E-02	BE567435.1	EST_HUMAN	601340681F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3983030 5'
8899	21865	35288	1.08	6.9E-02	BE567435.1	EST_HUMAN	601340681F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3983030 5'
9475	22430	35879	0.55	6.9E-02	U22967.1	NT	Barbican duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
12343	25141		2.17	6.9E-02	X74315.1	NT	X laevis XFD2 mRNA for fork head protein
12519	26250		1.75	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOPC HOMOLOG
13112	26631	31648	3.69	6.9E-02	BF352896.1	EST_HUMAN	IL3-HT0619-110700-210-C04 HT0619 Homo sapiens cDNA
1899	14924	27918	1.18	6.9E-02	AA456759.1	EST_HUMAN	as30102.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1899	14924	27919	1.18	6.9E-02	AA456759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1923	14948	27942	4.7	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3117	16174	29084	1.05	6.8E-02	AA781996.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds
3117	16174	29085	1.05	6.8E-02	AA781996.1	EST_HUMAN	at75a08.s1 Soares, testis, NHT Homo sapiens cDNA clone 1376528 3'
3117	16174	29086	1.05	6.8E-02	AA781996.1	EST_HUMAN	at75a08.s1 Soares, testis, NHT Homo sapiens cDNA clone 1376528 3'
4583	17605		0.71	6.8E-02	BE141076.1	EST_HUMAN	MRO-H10069-07069-001-c05 HT0069 Homo sapiens cDNA
5293	18289		0.76	6.8E-02	T03013.1	EST_HUMAN	FB20A6 Fetal brain, Stragena Homo sapiens cDNA clone FB20A6 3'end
6776	19831		0.66	6.8E-02	P20762	SWISSPROT	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
7084	20018		1.05	6.8E-02	BE061890.1	EST_HUMAN	RC1-B10254-060300-017-406 B10254 Homo sapiens cDNA
7497	20462	33822	7.18	6.8E-02	AL163269.2	NT	Homo sapiens chromosome 21 segment HS21C068
7948	20889	34280	0.84	6.8E-02	U16856.1	NT	Dicofatallum discoidium myosin heavy chain kinase A (MHCK A) mRNA, complete cds
8631	21599	35020	5.44	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
8631	21599	35021	5.44	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
12140	25949		3.73	6.8E-02	T03214.1	EST_HUMAN	FB4A8 Fetal brain, Stragena Homo sapiens cDNA clone FB4A8 3'end similar to LINE-1
12274	26094		2.52	6.8E-02	AA758014.1	EST_HUMAN	at6705.s1 Soares, testis, NHT Homo sapiens cDNA clone 1320705 3'
12832	28449		1.88	6.8E-02	AW975899.1	EST_HUMAN	EST1387848 MAGE cDNAs, MAGN Homo sapiens cDNA
12894	28480		2.35	6.8E-02	9610963	NT	Mus musculus latent TGF beta binding protein (ltgfb) mRNA
1531	14584		1.93	6.7E-02	AF115536.1	NT	Oncorhynchus mykiss TAP1 protein (OmnyTAP1) mRNA, OmnyTAP1.101 allele, complete cds
1910	14524	27930	1.90	6.7E-02	AJ220285.1	EST_HUMAN	q979e04.s1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841408 3'
3730	16772	29683	4.34	6.7E-02	P17276	SWISSPROT	HOMEOBOX PROTEIN HOXD4 (HOXD4)
8183	21153	34560	1.01	6.7E-02	X62665.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8183	21153	34561	1.01	6.7E-02	X62893.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8781	21748	33170	0.45	6.7E-02	AW092888.1	EST_HUMAN	X661c1.1.x1 Scores: N1L_T_GBC. S1 Homo sapiens cDNA clone IMAGE:2680788 3'
9559	22886	33347	0.73	6.7E-02	AW137359.1	EST_HUMAN	U1H-B11.acr-g01-01-U1.e1 N1L_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
9559	22886	36348	0.73	6.7E-02	AW137359.1	EST_HUMAN	U1H-B11.acr-g01-01-U1.e1 N1L_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1371	14405	27376	0.9	6.6E-02	AF245118.1	NT	Drosophila melanogaster cecin mRNA, complete cds
2192	16207	28228	2.68	6.6E-02	AJ289241.1	EST_HUMAN	Mus musculus Caprin2 gene for caprin 2, exons 1-21, three alternative transcripts
3477	16523	29447	11.07	6.6E-02	R64306.1	EST_HUMAN	yf18010.s1 Scores: placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3481	16537	29462	2.1	6.6E-02	7108357	EST_HUMAN	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3491	16537	29463	2.1	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4107	17141	30036	1.46	6.6E-02	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5015	18026	30913	9.23	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5015	18026	30914	9.23	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6736	19792	33073	3.97	6.6E-02	X06411.1	NT	P. vulgaris mRNA for chalcone synthase
6967	19823	33105	0.55	6.6E-02	P25156	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6967	19823	33106	0.55	6.6E-02	P25156	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
8162	21060		0.57	6.6E-02	D14667.1	NT	Penicillium urticae mitochondrial tRNA (large rRNA) gene and its flanking region
8279	21248	34650	1.6	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8517	21784	35209	0.67	6.6E-02	AF06055.1	NT	Dichytellum discoideum dar1in (darA) gene, complete cds
9273	22239	35666	0.67	6.6E-02	9629188	NT	Human respiratory syncytial virus, complete genome
9273	22239	35667	0.67	6.6E-02	9629188	NT	Human respiratory syncytial virus, complete genome
10311	23235	38717	0.52	6.6E-02	A1458752.1	EST_HUMAN	U97005.x1 N1L_CGAP_L124 Homo sapiens cDNA clone IMAGE:2149488 3'
10447	23369	38660	1.65	6.6E-02	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes
10481	23403		0.6	6.6E-02	11430569	NT	Homo sapiens vitruclin (VCL), mRNA
11310	24260	37766	4.9	6.6E-02	BF374248.1	EST_HUMAN	MRT-SN0064-01060-006-a12 SN0064 Homo sapiens cDNA
12063	24656		1.73	6.6E-02	C05789.1	EST_HUMAN	C05789 Human pancreatic islet Homo sapiens cDNA clone h051568
12719	25373		2.53	6.6E-02	9937991	NT	Mus musculus DIPB gene (DIPB), mRNA
13024	25572		1.31	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
584	13652	26566	2.67	6.5E-02	BF027639.1	EST_HUMAN	60167104G.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
585	14041	26836	1.95	6.5E-02	7706368	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1392	14426	27395	3.5	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1749	14778	27793	2.08	6.5E-02	AE000764.1	NT	Aquifex lewisii section 86 of 109 of the complete genome
6636	18724	31806	1.71	6.5E-02	AA443951.1	EST_HUMAN	z449H12.g1 Scores: ovary tumor hRbT1 Homo sapiens cDNA clone IMAGE:796743 3' similar to gbt/26038
6636	18750	33027	0.53	6.5E-02	BF565340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN); 602116687F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276029 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7165	18366	31241	1.17	6.5E-02	U23681.1	NT	Azotobacter vinelandii ATCC 35046 negative regulator MacB (nucB) gene, partial cds
10302	23227	38709	0.65	6.5E-02	BE963200.2	EST_HUMAN	601659817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10302	23227	38710	0.65	6.5E-02	BE963200.2	EST_HUMAN	601659817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10832	23763	37252	0.53	6.5E-02	BF106300.1	EST_HUMAN	601623911F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
11002	23968	37492	4.51	6.5E-02	AA195848.1	EST_HUMAN	z132905.61 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12164	25017		4.16	6.5E-02	M21466.1	NT	Rabbit microsomal epoxide hydrolase
12526	25255		7.31	6.5E-02	AF102983.1	NT	Nectria haemabocosa kinein related protein 2 (KRP2) gene, complete cds
577	13648	26559	1.74	6.4E-02	X94648.1	NT	A. canariensis precursor of perfrictin-chlorophyll-protein (PCP) gene
1746	14775	27760	0.93	6.4E-02	AE001777.1	NT	Thermococcus maritima section 88 of 138 of the complete genome
1748	14775	27761	0.93	6.4E-02	AE001777.1	NT	Thermococcus maritima section 88 of 138 of the complete genome
4833	15085	26007	1.16	6.4E-02	6596923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5282	18270		2.56	6.4E-02	AA147572.1	EST_HUMAN	z151604.1 Soares_pregnant_tissues_NIHMPU Homo sapiens cDNA clone IMAGE:504470 5' similar to contains Alu repetitive element;
5526	19624	31559	1.19	6.4E-02	AI191966.1	EST_HUMAN	q607601.X1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.63 LTR8 repetitive element;
5982	19067	32265	1.15	6.4E-02	7305186	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
6234	19307	32539	4.16	6.4E-02	AF052733.1	NT	Helicobacter glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6234	19307	32540	4.16	6.4E-02	AF052733.1	NT	Helicobacter glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6542	19604	32866	0.72	6.4E-02	AI872996.1	EST_HUMAN	we7g12.X1 Soares_Dickgraaf_cdon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
6590	20213	33542	4.84	6.4E-02	BE974448.1	EST_HUMAN	601660425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:38906003 3'
7893	20661	34015	0.52	6.4E-02	AL182757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
8879	21647		2.76	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (beta) (Cofa6), mRNA
9012	21978	35397	4	6.4E-02	AA063305.1	EST_HUMAN	141419 seq. F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9483	22447	35687	0.92	6.4E-02	AF150196.1	EST_HUMAN	AF150196 Homo sapiens mRNA from cd44+ stem cells Homo sapiens cDNA clone C8DAIA10
9644	22871		0.51	6.4E-02	BE834083.1	EST_HUMAN	RC1-OT0083-150600-014-g06 OT0083 Homo sapiens cDNA
10075	23002	36472	1.75	6.4E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10824	23546	37046	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 19, 17, and 18
10824	23546	37047	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
12018	24595	38492	2.18	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HHA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
12018	24595	38493	2.18	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HHA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12424	25861	31783	5.38	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
12476	25224	31783	5.88	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1769	14798	27794	2.76	6.3E-02	AF105905.1	NT	Mus musculus major histocompatibility locus class III regions Hae701 gene, partial cds; unRNP, G7A, NG23, HEAT homolog, CLOP, NG24, NG26, and NG26 genes, complete cds; and unknown genes
3618	16882	32563	2.77	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6269	19332	32563	1.06	6.3E-02	BF210738.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097489 5'
7453	20418	36038	1.39	6.3E-02	X97989.1	NT	H sapiens gene encoding La autoantigen
9646	22690	36038	1.01	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Drosophila gene, exons 1-3
10374	23297	36773	2.98	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-162
10634	23556	36773	0.81	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKGO Homo sapiens cDNA clone GKCAHE07 5'
11070	19332	32563	2.76	6.3E-02	BF210738.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097489 5'
4278	17307	30186	2.48	6.2E-02	AL161672.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 68
4365	17392		1.12	6.2E-02	AF271236.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4612	17633		6.56	6.2E-02	Q82191	SWISSPROT	52 KD RO PROTEIN(SJOGREN SYNDROME TYPE A ANTIGEN (SSA)) (RQ(S5-A)) (R052)
5963	20188	33513	0.87	6.2E-02	D49530.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7889	20833	34212	0.79	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8158	21096		0.98	6.2E-02	AL161645.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 45
9289	23037		0.53	6.2E-02	M81101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9699	22652	36106	0.53	6.2E-02	AA78460.1	EST_HUMAN	af20a06.s1 Soares, total, fetus, MS2HF8, 9w Homo sapiens cDNA clone IMAGE:1032178 3'
9835	22771	36228	1.25	6.2E-02		NT	Mus musculus stromal cell derived factor receptor 2 (Sdrf2), mRNA
12259	25879		15.68	6.2E-02	AE000750.1	NT	Aquifex mediterraneus section 82 of 109 of the complete genome
12598	25259		1.38	6.2E-02	BE783985.1	EST_HUMAN	601188373F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937842 5'
12876	25346	31784	3.54	6.2E-02	BF112839.1	EST_HUMAN	737708.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:352816 3' similar to
256	13353	28278	3.09	6.1E-02	D16471.1	NT	Human mRNA, Xa terminal portion
4017	17056		15.65	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds
6043	19126	32330	0.62	6.1E-02	7692463	NT	Arabidopsis thaliana K+ inward rectifying channel protein (KIAA1052), mRNA
6043	19125	32331	0.62	6.1E-02	7692463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
6235	19308		1.94	6.1E-02	4507070	NT	Homo sapiens SW/ISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8908	21674	34989	3.52	6.1E-02	X96268.1	NT	H sapiens mRNA for BHLH DNA binding protein
9009	21974	35393	1.93	6.1E-02	BE971853.1	EST_HUMAN	601661086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9008	21974	35394	1.93	6.1E-02	BE971853.1	EST_HUMAN	60165108RT NIH_MGC 81 Homo sapiens cDNA clone IMAGE:3934804 3'
11082	24044	37966	3.44	6.1E-02	BE176543.1	EST_HUMAN	IL3-IT0818-110500-138-C38 HT0818 Homo sapiens cDNA
12216	25897		2.42	6.1E-02	X70989.1	NT	S japonicum mRNA for serine-enzyme
12778	25774		1.35	6.1E-02	AI89691.1	EST_HUMAN	125907.x1 NC1_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2292901 3'
12912	26491		7.44	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C07
1297	14302	27263	1.25	6.0E-02	AE001777.1	NT	Thermoboga maritima section 89 of 136 of the complete genome
2684	15690	28608	1.17	6.0E-02	AW06948.1	EST_HUMAN	EST1300924 MAGE resources, MAGU Homo sapiens cDNA
							Mesocricetus corti mitochondrial DNA, NADH dehydrogenase subunit 4, rRNA-Gln, rRNA-Phe, rRNA-Met
2783	15775		1.96	6.0E-02	AB031289.1	NT	ATPase subunit 6, and NADH dehydrogenase subunit 2
2948	13213	26137	1.47	6.0E-02	AA189730.1	EST_HUMAN	2p78c04.r1 Stratagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:626310 5'
2948	13213	26138	1.47	6.0E-02	AA189730.1	EST_HUMAN	2p78c04.r1 Stratagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:626310 5'
3243	16298	29222	1.52	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3243	16298	29223	1.52	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
5472	18573		0.76	6.0E-02	AW370211.1	EST_HUMAN	RC3-870253-011199-013-b04 BT0253 Homo sapiens cDNA
							w48905.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains
6341	19410	32651	0.98	6.0E-02	A1807537.1	EST_HUMAN	L1.11 L1 repetitive element
7180	18411	31212	2.79	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7180	18411	31213	2.79	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7394	20962	33714	2.08	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4049228 5'
7508	20473	33833	0.57	6.0E-02	BF210468.1	EST_HUMAN	60184710F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4101074 5'
7844	20888	34277	1.71	6.0E-02	A1204275.1	EST_HUMAN	q53808.x1 Soares_testis NIH Homo sapiens cDNA clone IMAGE:1754198 3'
8765	21732		0.52	6.0E-02	11469495	NT	Recitomonas americana mitochondrion, complete genome
9627	22571	36020	1.17	6.0E-02	A623167.1	EST_HUMAN	1678a05.x1 NC1_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237362 3'
9627	22571	36021	1.17	6.0E-02	A1623167.1	EST_HUMAN	1678a05.x1 NC1_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237362 3'
9761	22702	36159	2.03	6.0E-02	A1245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9761	22702	36160	2.03	6.0E-02	A1245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
							EST1180954 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
10285	23160	36675	0.66	6.0E-02	AA309797.1	EST_HUMAN	EST1180954 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
10285	23160	36676	0.66	6.0E-02	AA309797.1	EST_HUMAN	EST1180954 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
12475	25223	31792	3.08	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12845	25455		3.16	6.0E-02	A1806273.1	EST_HUMAN	w65h33.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360985 3' similar to TR-O60298
232	13332	26256	5.34	5.8E-02	AW834718.1	EST_HUMAN	O60298 KIAA0051 PROTEIN
							RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2996	16054	28975	3.42	5.9E-02	AF190289.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4905	17922	30814	0.94	5.9E-02	AF096304.1	NT	Secharchomys cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
7077	25674	33409	0.62	5.9E-02	AF145980.1	NT	Drosophila melanogaster LD23197 wing (slmg) mRNA, complete cds
8984	21970	33355	1.82	5.9E-02	9056249	NT	Mus musculus trochantin related homeobox 3 (Drosophila) (trh3), mRNA
9809	21128		0.22	5.9E-02	BF242748.1	EST_HUMAN	60187609F1 NIH_MGC_S5 Homo sapiens cDNA clone IMAGE:4105994 5'
11138	24098		3.23	5.9E-02	6879870	NT	Mus musculus follistatin-like (Fstl), mRNA
933	13986		6.03	5.9E-02	D60110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
2872	15832		0.99	5.9E-02	AJ223821.1	NT	Populus trichocarpa CCAOMT1 gene, exon 1 to exon 5
3678	19719	29633	1.32	5.9E-02	AE001775.1	NT	Thermotoga maritima section 87 of T38 of the complete genome
4382	17410	30292	5.33	5.9E-02	AW051927.1	EST_HUMAN	w24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4382	17410	30293	5.33	5.9E-02	AW051927.1	EST_HUMAN	w24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4578	17600	30495	4.73	5.9E-02	AJ247595.1	EST_HUMAN	q15691.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1846897 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4578	17600	30496	4.73	5.9E-02	AJ247595.1	EST_HUMAN	q15691.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1846897 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4904	17625		2.93	5.9E-02	AF090264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6014	19097	32298	0.63	5.9E-02	AA190994.1	EST_HUMAN	z988a11.s1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627068 3'
7941	20893	34273	2.52	5.9E-02	M69150.1	NT	Human polymorphic microsatellite DNA
7941	20893	34274	2.52	5.9E-02	M69150.1	NT	Human polymorphic microsatellite DNA
9014	21980	35396	0.59	5.9E-02	AL163265.2	NT	Homo sapiens chromosome 21 segment HS21C0683
12955	25568		10.6	5.9E-02	AA604269.1	EST_HUMAN	nc78a11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3070	16127	29039	1.27	5.7E-02	A051644.1	EST_HUMAN	q163b05.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP-C37A2.2
3088	18143	29055	1.51	5.7E-02	AF119117.1	NT	CE08811;
3814	18854	29781	2.47	5.7E-02	AW066791.1	EST_HUMAN	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
5169	18208	31032	0.91	5.7E-02	AJ251673.1	NT	EST1378965 MAGIE resequences, MAGI Homo sapiens cDNA
5306	18308		1.18	5.7E-02	6754525	NT	Homo sapiens partial strophin-1 gene
5378	19084		0.69	5.7E-02	AF275948.1	NT	Mus musculus low density lipoprotein receptor (Ldlr), mRNA
7704	20681	34025	0.69	5.7E-02	BE871911.1	EST_HUMAN	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7704	20681	34026	0.69	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3951985 5'
7769	20739	34111	0.68	5.7E-02	D78003.1	NT	601447937F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3951985 5'
7769	20739	34112	0.68	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8495	21463	34879	1.74	5.7E-02	AJ266080.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
10209	23134	36621	0.65	5.7E-02	6681260	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv2.2 gene)
							Mus musculus ec2 oncogene (Ect2), mRNA

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10930	23850	37365	0.49	5.7E-02	Z49963.1	NT	L.mexicana cpb1 gene
11521	24462	38013	3.22	5.7E-02	AI752885.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11521	24462	38014	3.22	5.7E-02	AI752885.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11676	24942		1.89	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
12573	25782		8.27	5.7E-02	D50320.1	NT	Pig DNA for SPN12, complete cds
12794	25855		3.72	5.7E-02	AF217490.1	NT	Homo sapiens fragile T6D oddo reductase (FOR) gene, exons 8, 9, and partial cds
12930	25658		5.65	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
1529	14562	27533	1.85	5.6E-02	AF094455.1	NT	Hydroxycyde rotundifolia ribosomal protein L16 (p16) gene, intron; chloroplast gene for chloroplast product
4671	17692	30578	1.92	5.6E-02	AB013100.1	NT	Lycopodium seculentum LE-ACS5 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4725	17745	30636	1.21	5.6E-02	AA290599.1	EST_HUMAN	z45c01.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6817	19871	33100	5.93	5.6E-02	AW172708.1	EST_HUMAN	KIA09065 PROTEIN. ;
7075	20097	33407	0.77	5.6E-02	AA866182.1	EST_HUMAN	od47712.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7358	20328	33677	2.94	5.6E-02	BE008001.1	EST_HUMAN	QV0-BN0147-280400-214-g07 BN0147 Homo sapiens cDNA
8141	21078	34478	0.91	5.6E-02	AI183883.1	EST_HUMAN	q464111.X1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1734308 3'
9154	22120	35548	2.47	5.6E-02	BE642663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
9154	22120	35549	2.47	5.6E-02	BE642663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
10171	23096	36576	1.06	5.6E-02	AA482964.1	EST_HUMAN	LAMINA ASSOCIATED POLYPEPTIDE 1C. ;
11891	24772		1.87	5.6E-02	AF260226.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2663	15660	28878	8.23	5.5E-02	X87889.1	NT	H sapiens gene encoding La autoantigen
3228	16283	29207	3.44	5.5E-02	6756501	NT	Mus musculus Sfr3 domain protein 1b (Sfr3b), mRNA
4244	17273	30157	1.13	5.5E-02	L41561.1	NT	Gallid herpesvirus mRNA fragment
5742	18336	32017	3.09	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6141	18336	32017	3.81	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7603	20564	33925	1.85	5.5E-02	6755802	NT	Mus musculus tubulin 1 (Tub1), mRNA
8457	21426	34842	0.69	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8457	21426	34843	0.69	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
10013	22940	36405	0.63	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10013	22940	36408	0.63	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
10107	23033	36510	1.45	6.5E-02	U69482.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
11360	24309	37855	6.48	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, peridol cda, dihydroxyacetone kinase (dhak), glycerol dehydrogenase (dhGD), transcriptional activator (dhaT), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >
13089	25920	31303	1.99	5.5E-02	11421332	NT	Homo sapiens hypothetical protein SRRP-52 (SRRP-52), mRNA
3032	18090		1.02	5.4E-02	AJ277468.1	NT	Oryza sativa Rb45-1 gene for putative Bowman Birk trypsin inhibitor
3433	18323		0.97	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0558-140200-012-033 BT0558 Homo sapiens cDNA
3831	18971	28885	0.7	5.4E-02	U65806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8462	21431		1.05	5.4E-02	Z89118.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2385281 to 2813730
8426	22390	35828	0.53	5.4E-02	AF260226.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
11057	24020	37543	1.54	5.4E-02	U20790.1	NT	Neurospora crassa ubiquitin-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
1056	14102	27052	1.91	5.3E-02	AW391248.1	EST_HUMAN	QVO-ST0213-021289-062-508 ST0213 Homo sapiens cDNA
1096	14102	27053	1.91	5.3E-02	AW391248.1	EST_HUMAN	QVO-ST0213-021289-062-508 ST0213 Homo sapiens cDNA
1506	14539	27511	16.63	5.3E-02	T94759.1	EST_HUMAN	yca37112.1 Streptococcus pneumoniae (492) ST0213 Homo sapiens cDNA clone IMAGE:119851 5' similar to gb:K01508
2504	15507	28533	2.12	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2953	16011	28937	0.95	5.3E-02	M58417.1	NT	Pseudomonas putida tgs gene
2953	16011	28938	0.95	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3167	19222	29137	5.38	5.3E-02	AJ276408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
4841	17692	30550	0.9	5.3E-02	AJ011046.1	NT	Pseudomonas putida tgs gene
5125	18134	31011	8.41	5.3E-02	M80463.1	NT	Arabidopsis thaliana ellis gene, exons 1-11
5392	18495	31372	1.8	5.3E-02	AE000527.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5392	18495	31373	1.8	5.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
6222	19296	32530	3.03	5.3E-02	M85289.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
7088	20090	33398	3.94	5.3E-02	U095413	NT	Human hepatitis surface proteoglycan (HSPG2) mRNA, complete cds
7298	20271	35606	1.23	5.3E-02	U32832.1	NT	Lymphocytis disease virus 1, complete genome
7585	20548		2.12	5.3E-02	S78231.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
8209	21108	34507	0.51	5.3E-02	P38742	SWISSPROT	nuclear protein TIF1 isoform (mice, mRNA, 4063 nt)
8748	21716		0.5	5.3E-02	U10098.1	NT	HYPOPHYSAL 130.0 KD PROTEIN IN SNF6-SP011 INTERGENIC REGION
9481	22445	35986	2.05	5.3E-02	X03127.1	NT	Mus musculus 129/Sv. cystatin C (cat3) gene, complete cds
10497	23413	38971	0.61	5.3E-02	AB022805.1	NT	Podocarpus neriifolius mitochondrial atp6a gene, complete cds
10491	23413	38972	0.61	5.3E-02	AB022805.1	NT	Homo sapiens hCOMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)
10491	23413	38972	0.61	5.3E-02	AB022805.1	NT	Homo sapiens hCOMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)





Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12699	25359		1.75	5.1E-02	AF062467.1	NT	Cucurbita melo polygalacturonase precursor (MPG3) mRNA, complete cds
12691	25311		1.6	5.1E-02	AA33104.1	EST_HUMAN	R73902.ct NCL_CGAP_P10 Homo sapiens cDNA clone IMAGE:598139
12681	13556	26481	2.16	5.0E-02	AF080004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
935	13558	26938	4.95	5.0E-02	Z33896.1	NT	O. virginianus (HEL37) microsatellite DNA
1209	14247	27205	4.03	5.0E-02	Z59104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213980
2007	15028	28036	4.94	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FPIF-3) (PROTEIN APTROIN C) [CONTAINS: PEPTIDE P-C]
2828	14040	26995	1.62	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3348	16359		1.34	5.0E-02	7305610	NT	Mus musculus Uro-51 like kinase 2 (C. elegans) (UK2), mRNA
3609	16654		1.01	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 87 of 163 of the complete genome
3659	16739	29552	13.62	5.0E-02	U12769.2	NT	Archaea permy period clock protein homolog mRNA, complete cds
6253	18328	32557	0.77	5.0E-02	AF096284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6441	18508		1.25	5.0E-02	AJ242623.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7161	18412	31214	0.6	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
7765	20738	34110	12.03	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
8008	20948		0.52	5.0E-02	AW062464.1	EST_HUMAN	MK-CT0064-100899-002-g10 CT0064 Homo sapiens cDNA
10960	23482	36977	1.26	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fik3) mRNA, complete cds
11920	24703	38285	2.47	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
12226	26518		6.4	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
226	13325		27.81	4.9E-02	M14220.1	NT	Chicken 28-3Da vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
369	13455	26384	2.96	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
369	13455	26385	2.96	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3302	16355	29274	1.64	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL PALIDOLUTYSIAN ATROPHY PROTEIN)
3584	16629		0.7	4.9E-02	AA188940.1	EST_HUMAN	2q4812.s1 Striatum INT neuron (#637233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element; contains element MSRT1 repetitive element;
3605	16650	29966	0.96	4.9E-02	AA400914.1	EST_HUMAN	278d03.s1 Scare, testis, NHT Homo sapiens cDNA clone IMAGE:729428 3'
3605	16650	29967	0.96	4.9E-02	AA400914.1	EST_HUMAN	278d03.s1 Scare, testis, NHT Homo sapiens cDNA clone IMAGE:729428 3'
4877	17894	30783	2.11	4.9E-02	AW167821.1	EST_HUMAN	Xg56g10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632366 3'
4877	17894	30784	2.11	4.9E-02	AW167821.1	EST_HUMAN	Xg56g10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632366 3'
5444	18546	31459	1.71	4.9E-02	U01122.1	NT	Rat alkalase II gene, exon 6
5444	18546	31459	1.71	4.9E-02	U01122.1	NT	Rat alkalase II gene, exon 6
7346	20319	33666	2.83	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8963	21029		0.81	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 95 of the complete genome
6107	22073	35590	0.8	4.9E-02	AL161569.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10556	23578	37075	0.53	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
11730	24518	38193	3.44	4.9E-02	AF08303.1	NT	Homo sapiens prepro pituitary TGF-beta gene, complete cds
12879	25473		6.66	4.8E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
330	13420	28344	1.06	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
331	13420	28344	2.41	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
489	13562	20486	12.99	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2281	15294	28318	2.24	4.8E-02	W51983.1	EST_HUMAN	z44902.s1 Soares, senescent, fibroblasts NIH3T3 Homo sapiens cDNA clone IMAGE:325611 3' similar to gb X60538 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3222	16277	29202	1.83	4.8E-02	X17144.1	NT	Tetrahymena costata histone H3.1 and histone H4.1 intergenic DNA
4698	17718		1.24	4.8E-02	Z54280.1	NT	S. acrofa gene for skeletal muscle myosin receptor
5174	18183	31060	0.63	4.8E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
8477	21446	34863	1.55	4.8E-02	AW398497.1	EST_HUMAN	MR2-ST0129-227069-072602 ST0128 Homo sapiens cDNA
9485	22449	35689	0.76	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9485	22449	35690	0.76	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
12505	25242		1.35	4.8E-02	9632893	NT	Streptococcus thermophilus bacteriophage Sfi18, complete genome
7004	20130	33445	3.77	4.7E-02	W01153.1	EST_HUMAN	y29709.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element;
7069	20091	33396	0.88	4.7E-02	BF68625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7069	20091	33400	0.88	4.7E-02	BF68625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7103	20037	33340	1.66	4.7E-02	M62752.1	NT	Rat salivary-related protein (s1) gene, complete CDS
8594	21682	34976	8.96	4.7E-02	X15543.1	NT	B. taurus mRNA for Rf-38-DNA-binding protein
9305	22270	35701	1.65	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9327	22292		2.51	4.7E-02	AB028678.1	NT	Gallus gallus Wpico-8 gene, complete cds
9582	22541	35995	7.94	4.7E-02	X15543.1	NT	B. taurus mRNA for Rf-38-DNA-binding protein
10035	22932	36395	0.55	4.7E-02	BF305237.1	EST_HUMAN	601892682F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
10092	23018		0.96	4.7E-02	A1873042.1	EST_HUMAN	wef9c10.x1 Soares_MFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
12783	25970		1.97	4.7E-02	P52651	SWISSPROT	HOMEOBOX PROTEIN GBX2 (GASTRULATION AND BRAIN-SPECIFIC HOMEOBOX PROTEIN 2)
13022	25570		1.56	4.7E-02	AJ277862.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
270	13866	28292	1.08	4.6E-02	BE163853.1	EST_HUMAN	PMCHT0339-261189-003-g05 HT0339 Homo sapiens cDNA
741	13862	28741	3.47	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1361	14365	27366	3.62	4.6E-02	AV727059.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBW C01 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2496	15499	28525	4.32	4.6E-02	AW236023.1	EST_HUMAN	xn24f03.x1 NC1, CGAP K1611 Homo sapiens cDNA clone IMAGE:2894653 3' similar to SW:GRF1_HUMAN
2819	13566	26282	1.03	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1:
3020	16078	28999	0.87	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3342	16078	28999	0.67	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3307	16078	28999	0.91	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4149	17180		1.24	4.6E-02	AF220365.1	NT	Mus musculus nucleolar RNA helicase II(Gu ddx21) gene, complete cds
5252	18260	31126	0.84	4.6E-02	AA079157.1	EST_HUMAN	gb:X02012 KERPATIN, TYPE II CYTOSKELETAL 7 (HUMAN);
5823	18913	32096	1.42	4.6E-02	AF076962.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
6357	19426	32658	4.48	4.6E-02	X61624.1	NT	C.reinhardtii apb2 (apb3) mRNA
6357	19426	32658	4.48	4.6E-02	X61624.1	NT	C.reinhardtii apb2 (apb3) mRNA
6968	20191	33518	1.51	4.6E-02	AI149574.1	EST_HUMAN	q60606.X1 Soares, placenta, 8to8weeks, 2NHFP8to8W Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1.13 L1 repetitive element :
8134	21071	34470	0.96	4.6E-02	6978720	NT	Rattus norvegicus Cathelin H (Cish), mRNA
9003	21969	35391	2.89	4.6E-02	BE154006.1	EST_HUMAN	PMO-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
11731	24517	38194	5.31	4.6E-02	AA913328.1	EST_HUMAN	cd27009.s1 Soares, NFL_L1, GBC, S1 Homo sapiens cDNA clone IMAGE:1524737 3'
12761	25987		1.99	4.6E-02	L11692.1	NT	Oryzias latipes macrophage scavenger receptor type II mRNA, complete cds
12992	25552		8.41	4.6E-02	X57608.1	NT	Human germine immunoglobulin lambda light chain gene
437	13520	28453	1.9	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1222	14260	27217	0.78	4.5E-02	AF05730.1	NT	Marburg virus strain MIS Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1222	14260	27218	0.78	4.5E-02	AF05730.1	NT	Marburg virus strain MIS Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1821	14948	27841	4.23	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2119	15136	28156	3.34	4.5E-02	AE003964.1	NT	Xyella fastidiosa, section 110 of 229 of the complete genome
3736	18778	29691	4.42	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6358	19427	32670	1.63	4.5E-02	AJ400877.1	NT	Homo sapiens ASC.3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene and C11orf17 gene
6658	19713	32960	0.94	4.5E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7062	20084	33392	0.96	4.5E-02	L26487.1	NT	Methanocaldococcus JFida carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
7062	20084	33393	0.96	4.5E-02	L26487.1	NT	Methanocaldococcus JFida carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
8736	21704	35128	2.34	4.5E-02	AF036884.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10309	23233	38715	4.58	4.5E-02	AA325218.1	EST_HUMAN	EST28167 Cerebellum, il Homo sapiens cDNA 5' end similar to neuro-D4 protein
10450	23382	38875	0.43	4.5E-02	X05508.1	NT	A. aureum mRNA for leucine-like protein
10577	23469	39591	0.81	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12440	25203	31826	2.95	4.5E-02	11418013	NT	Homo sapiens rat finger protein-like 3 (RPPL3), mRNA
12823	23663	31440	7.3	4.5E-02	AA191097.1	EST_HUMAN	z443971.1 Slc1a2 gene, Homo sapiens cDNA clone IMAGE:632493 5'
222	12322	15822	4.84	4.4E-02	BE072733.1	EST_HUMAN	601662154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2107	15124		8.38	4.4E-02	P31568	SWISSPROT	HYPOPHOSPHATE PROTEIN (ORF 2280)
2498	15501	28527	2.11	4.4E-02	AW87475.1	EST_HUMAN	QV24P10072-010300-070-g02 PT0012 Homo sapiens cDNA
3854	16597	29612	2.01	4.4E-02	AF159160.1	NT	Mycoplasma xanthus serine/threonine kinase Pln10 (pln10) gene, complete cds
4657	17678	30563	1.25	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PST and hypothetical protein genes, complete cds; and S171 gene, partial cds
4657	17678	30564	1.25	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PST and hypothetical protein genes, complete cds; and S171 gene, partial cds
4771	17791		0.94	4.4E-02	AJ222889.1	NT	Ovis aries CCAAT-enhancer binding protein epsilon gene
7325	20296	33639	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7325	20296	33640	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
9105	22071	35407	2.17	4.4E-02	AA736969.1	EST_HUMAN	nm13103.st NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11409	24353	37886	3.75	4.4E-02	AF060659.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
11533	24474	38025	2.56	4.4E-02	AA496739.1	EST_HUMAN	sa3304.4.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
12159	25014		2.22	4.4E-02	AB040928.1	NT	Homo sapiens mRNA for KIAA1453 protein, partial cds
12346	25980		1.83	4.4E-02	BF21245.1	EST_HUMAN	601878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
7871	13841	26786	5.93	4.3E-02	AF003246.1	NT	Merone axonitis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2875	15576	28595	1.4	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAO108 5'
3443	18490	29409	6.93	4.3E-02	AF163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3671	18714		1.25	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5644	19702	32977	4.62	4.3E-02	P30427	SWISSPROT	PLECTIN
6644	19702	32978	4.62	4.3E-02	P30427	SWISSPROT	PLECTIN
6808	19948	33245	0.73	4.3E-02	AA65226.1	EST_HUMAN	ms86c12.st NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:118886
8958	21625	35248	0.9	4.3E-02	AF28359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
9153	22119	35546	0.95	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
9153	22119	35547	0.95	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
823	13881	29832	1.85	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
867	13923		2.58	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
897	13652	28910	0.83	4.2E-02	AW003645.1	EST_HUMAN	w34q01.x1 NCL CGAP_P111 Homo sapiens cDNA clone IMAGE:2545684.3 similar to TR-Q83291 Q83291
1733	14763		1.54	4.2E-02	AL445066.1	NT	L1 RETROPOSON, ORF2 mRNA, contains L1.03 L1 repetitive element ;
1783	14822	27806	1.02	4.2E-02	P23091	SWISSPROT	Thermoplasma acidophilum complete genome; segment 4/5
3677	16720	28634	2.18	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4774	17794	30686	0.73	4.2E-02	BF342965.1	EST_HUMAN	602017105F1 NCL CGAP_Bnc61 Homo sapiens cDNA clone IMAGE:4152672.5
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31957	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31958	0.85	4.2E-02	AF280107.1	NT	4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds
1775	18405	31205	0.73	4.2E-02	BE288265.1	EST_HUMAN	601124598F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2886318.5
7789	20722	34094	4.52	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7793	20745	34118	0.61	4.2E-02	AV730347.1	EST_HUMAN	AV730347 HTF Homo sapiens cDNA clone HTFAVH04.5
8162	22128	35556	3.74	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ.3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10525	23447	36045	1.19	4.2E-02	Q16850	SWISSPROT	T-BRAIN-1 PROTEIN (T-BRAIN PROTEIN 1) (TBR-1) (TES-58)
11379	24326	37655	1.58	4.2E-02	AA976118.1	EST_HUMAN	on33b11.s1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1958461.3 similar to gb:M65280
11637	24574	38138	2.65	4.2E-02	BE815822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11637	24574	38139	2.65	4.2E-02	BE815822.1	EST_HUMAN	PM3-BND174-250500-009-410 BN0174 Homo sapiens cDNA
12594	25608		5.62	4.2E-02	AI953464.1	EST_HUMAN	W40g10.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850.3
12990	25550		1.69	4.2E-02	D14711.1	NT	Saprophyococcus aureus HSP10 and HSP60 genes
511	13582	28503	0.75	4.1E-02	AF206826.1	NT	Homo sapiens HSP51 gene, Intron 5
2965	15631	28669	1.18	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 80 of 85 of the complete genome
4499	17524		7.84	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-160400-164-06 NND012 Homo sapiens cDNA
5302	18305	31169	0.82	4.1E-02	5602103	NT	Homo sapiens SRY (sex-determining region Y)-box 10 (SOX10), mRNA
5726	18820	31698	1.08	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3343856.5
5726	18820	32000	1.08	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3343856.5
7068	20098		0.9	4.1E-02	X75681.1	NT	A. thaliana mRNA for plasma membrane intrinsic protein 1a
7306	20277	33615	1.19	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7756	20709	34078	2	4.1E-02	7662347	NT	Homo sapiens KIAA0887 protein (KIA0887), mRNA
							Mus musculus proviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, Intron 1, with the proviral insert encompassing the env pseudogene (3' end) 3' LTR
7960	20804	34180	0.7	4.1E-02	L0210.1	NT	

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8042	20978	34375	2.53	4.1E-02	AF026108.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and cadherin channel alpha-1 subunit>
8549	21517	34535	0.58	4.1E-02	P97857	SWISSPROT	ADAM-11 (ADAMTS-1) (ADAM-TS1)
8550	21956	35381	0.57	4.1E-02	P34687	SWISSPROT	GUTILE COLLAGEN 34
9509	22472	35916	0.83	4.1E-02	AJ372598.1	EST_HUMAN	Hs42821 Capon adenocarcinoma IV Homo sapiens cDNA 5' end
13013	25909	31423	4.48	4.1E-02	AJ271909.1	NT	Brassicale napus glin gene for plastid glutamine synthetase, exons 1-12
13102	25625	31879	1.33	4.1E-02	AF254922.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
1649	14681	27854	1.21	4.0E-02	AF675392.1	EST_HUMAN	wb9b01.x1 NCI CGAP P28 Homo sapiens cDNA clone IMAGE2313745.3
3258	16312	26233	2.57	4.0E-02	AB040004.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
5453	18555	31466	5.39	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6339	19408	32849	1.43	4.0E-02	BF110434.1	EST_HUMAN	7n52h07.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE3568380.3 similar to TR O75296 O75296 R20124.1..
7854	20895	34288	6.1	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
8026	20963		0.58	4.0E-02	AL161335.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
8043	20980	34376	0.85	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8043	20980	34377	0.85	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
9087	22033	35456	2.78	4.0E-02	P06940	SWISSPROT	GLUCAMYLASE STS2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCO)HYDROLASE
10022	22529		0.71	4.0E-02	BF676576.1	EST_HUMAN	602153894F1 NIH MGSC_83 Homo sapiens cDNA clone IMAGE4294724.5
10027	22954	36423	2.95	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiol fumarate reductase subunit A
10344	23268		0.92	4.0E-02	D43346.1	NT	Human mRNA for KIAA0082 gene, partial cds
12088	24941		1.48	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Cse** ATPase
12331	25790	31614	3.52	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1122	14166	27118	3.13	3.9E-02	BF516149.1	EST_HUMAN	UH-BW 1-arc-H08-QJ1st NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE3084134.3
1348	14383	27351	1.9	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1978	14959	28001	2.82	3.9E-02	AJ403386.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2715	15709		2.12	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5191	19200	31072	0.65	3.9E-02	AW392417.1	EST_HUMAN	RC6-ST0258-171199-021-C06 ST0258 Homo sapiens cDNA

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5573	18659	31630	0.74	3.9E-02	D96098.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5573	18659	31631	0.74	3.9E-02	D96098.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5820	18810	32094	1.08	3.9E-02	BE98694.1	EST_HUMAN	601649874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933842 5'
5957	19042	32241	0.71	3.9E-02	BF675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7259	18984	33291	1.1	3.9E-02	BE271437.1	EST_HUMAN	601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3046830 5'
8167	21105	34504	0.63	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
8172	21142	34548	1.07	3.9E-02	BF239613.1	EST_HUMAN	60190848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134778 5'
8393	21364	34772	0.63	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8393	21364	34773	0.63	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11737	21105	34504	1.61	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
12184	28972		14.17	3.9E-02	A9042953.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12648	25704		6.15	3.9E-02	ALD49866.2	NT	Mus musculus chromosome X contig81; X-linked lymphocyte regulated 5 gene, Zinc finger protein 2/5, Zinc finger protein 82, mrx2Borf
1968	14990	27993	1.13	3.9E-02	BE985137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'
2129	15148		1.1	3.9E-02	AJ251973.1	NT	Homo sapiens partial atserm-1 gene
4906	17923	30815	0.92	3.9E-02	BE393275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3628767 5'
4906	17923	30816	0.82	3.9E-02	BE393275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3628767 5'
4985	17980	30870	1.4	3.9E-02	AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM200 698 5'
5515	18615	31548	1.2	3.9E-02	M11228.1	NT	Human protein G gene, complete cds
6205	16280	32513	1.04	3.9E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOXB4 (HOX-2.6)
7540	20503	33662	1.43	3.9E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC), member 8 (ABCA8), mRNA
9011	21977		1.26	3.9E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
11014	23979	37505	2.04	3.9E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
12009	24886	39481	1.53	3.9E-02	P01641	SWISSPROT	IG KAPPA CHAIN V-Y REGION MOPC 17B3 PRECURSOR
12009	24886	39482	1.53	3.9E-02	P01641	SWISSPROT	IG KAPPA CHAIN V-Y REGION MOPC 17B3 PRECURSOR
994	14045	26969	4.76	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1389	14423	27392	0.98	3.7E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2245	15260	26287	4.98	3.7E-02	A084806.1	EST_HUMAN	w858c03.v1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
3065	16120	28034	1.27	3.7E-02	P78944	SWISSPROT	IONOSODERMIN
3065	16122	28035	4.14	3.7E-02	BF312963.1	EST_HUMAN	601898233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126594 5'
3468	16514		1.03	3.7E-02	6680541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
5279	18285	31148	0.76	3.7E-02	AF168106.1	NT	Bubo virginianus cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product



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7281	25398		0.79	3.7E-02	AF000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
7956	20897	34290	0.64	3.7E-02	AE003975.1	NT	Xyella fastidiosa, section 121 of 239 of the complete genome
10375	23298		0.99	3.7E-02	AA782516.1	EST_HUMAN	xl55c09.a1 Soares parathyroid tumor NIH/PA Homo sapiens cDNA clone IMAGE:1360912 3'
12225	25061	38628	5.94	3.7E-02	BF124974.1	EST_HUMAN	60176217F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024873 5'
12883	25762	31820	2.34	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3657	16710	29625	1.04	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3674	16717	29631	0.75	3.6E-02	AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5253	18261	31130	2.27	3.6E-02	AL096810.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5501	18601	31514	0.8	3.6E-02	X59403.1	NT	C. glutamicum gap, polk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5501	18601	31530	0.8	3.6E-02	X59403.1	NT	C. glutamicum gap, polk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5578	18674	31638	0.88	3.6E-02	AF161722.1	NT	Homo sapiens RUTAS (RUT) mRNA, complete cds
6855	19818	33212	4.97	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192.b10 EN0013 Homo sapiens cDNA
6855	19818	33213	4.97	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192.b10 EN0013 Homo sapiens cDNA
7150	18382	31270	0.5	3.6E-02	U67575.1	NT	Methanococcus jannaschii section 117 of 150 of the complete genome
7291	20263	33597	1.7	3.6E-02	AF025962.1	NT	Chromatium vinosum sulfur globule protein OX2 precursor (sgp2) gene, complete cds
7527	20491	33853	2.75	3.6E-02	AA714621.1	EST_HUMAN	hw20a5.a1 NCI_QGAP_QG30 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:U00314_me2
7895	20538	34218	1.08	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
8746	22687	36142	1.85	3.6E-02	U20608.1	NT	MRQ-HT0158-030200-003-b08 HT0158 Homo sapiens cDNA
8745	22687	36143	1.85	3.6E-02	U20608.1	NT	Dicystatium discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
8971	22898	36361	0.88	3.6E-02	BF347586.1	EST_HUMAN	602020453F1 NCI_QGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158116 5'
898	13951	26909	0.9	3.5E-02	U09506.1	NT	Drosophila melanogaster tigrilin mRNA, complete cds
1010	14059	27011	1.38	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1566	14569	27574	1.3	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:1248377 5'
1566	14569	27575	1.3	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:1248377 5'
4241	17270	30155	1.95	3.5E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome
4344	17371	30253	3.67	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5265	18273		1.04	3.5E-02	P47144	SWISSPROT	HYPOTHETICAL 80.7 KD PROTEIN IN SOD1-CPA2 INTERGENIC REGION
6347	19416	32857	1.74	3.5E-02	J01238.1	NT	Maize actin 1 gene (MaAct), complete cds
8310	21279		0.78	3.5E-02	H28951.1	EST_HUMAN	Yp44405.r1 Soares retina N2b3HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element.
8970	21836	35362	2.87	3.5E-02	BE938970.1	EST_HUMAN	60164701.R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929737 3'
10378	23301	36771	1.99	3.5E-02	X76942.1	NT	L1aetis MG1383 gfpE and oneK genes
10425	23347	39632	0.47	3.5E-02	BE561042.1	EST_HUMAN	60134461.F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11823	24706	39288	1.61	3.5E-02	AW851641.1	EST_HUMAN	PM1-C10326-291299-02-103 C10326 Homo sapiens cDNA
11823	24706	39288	1.61	3.5E-02	AW851641.1	EST_HUMAN	PM1-C10326-291299-02-103 C10326 Homo sapiens cDNA
12877	26808		5.77	3.5E-02	BE276948.1	EST_HUMAN	601178765.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
580	13649	28662	0.91	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ000013 protein, partial cds
580	13649	28662	0.91	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ000013 protein, partial cds
581	13649	28592	3.42	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ000013 protein, partial cds
581	13649	28592	3.42	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ000013 protein, partial cds
1053	14098	27049	2.4	3.4E-02	AW274020.1	EST_HUMAN	xv2607.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814293 3' similar to SW-C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1211	14249		6.51	3.4E-02	11345469	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2401	15408	28432	2.51	3.4E-02	T57160.1	EST_HUMAN	yc20e06.r1 Strelasene lung (#837210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER25 repetitive element
3444	18461	28410	1.19	3.4E-02	AL183208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3942	16982	28897	3.71	3.4E-02	AW784952.1	EST_HUMAN	RC5-UM0015-210200-02-1-A10 UM0015 Homo sapiens cDNA
4829	17649	30637	3.05	3.4E-02	X56769.1	NT	M.musculus S-antigen gene promoter region
5100	18110		2.48	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5114	18124	30998	1.93	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6330	19400		0.93	3.4E-02	BF131628.1	EST_HUMAN	601820445.F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052434 5'
7032	18364	31251	3.97	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8604	21572		3.14	3.4E-02	AI859529.1	EST_HUMAN	wb9d04.x1 NC1 CGAP_AIV1 Homo sapiens cDNA clone IMAGE:2433031 3'
8100	22086	35492	1.58	3.4E-02	AA694986.1	EST_HUMAN	element contains element MER25 MER25 repetitive element ;
							zq04f1.s1 Stratiogene muscle 937206 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
9268	22234		6.2	3.4E-02	AA194306.1	EST_HUMAN	IPISGKPLKPVTLSRDGVPLKATMRNFTEITAEINTLNKESVYATDAGRYEITTAANSSTGTTKAFINWLDPRP-G
10135	23062		0.64	3.4E-02	A082719.1	EST_HUMAN	PPT GPVVISDITSESVTLTKWPKPYDGSQVNTYLLIKRSTAVTVTSATVARTMMKMKL ... ;
							ozb8h08.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1693519 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
372	13458		9.24	3.3E-02	AA398735.1	EST_HUMAN	z175c08.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1171	14212	27168	14.49	3.3E-02	AB039807.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1845	14677	27650	1.73	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (HLI) gene, complete cds
1753	14782		1.29	3.3E-02	AE000700.1	NT	Aquifex naeclius section 32 of 109 of the complete genome
2096	15173		1.76	3.3E-02	R09112.1	EST_HUMAN	y125c08.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:127688 5'
2458	15462	28485	1.31	3.3E-02	6755962	NT	Mus musculus tumor rejection antigen gp98 (Trt1), mRNA
3272	16422	26347	8.85	3.3E-02	H024389.1	EST_HUMAN	y135r02.1 Soares placenta N24P2P Homo sapiens cDNA clone IMAGE:150771 5'
4305	14677	27650	2.38	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (HLI) gene, complete cds
4494	17818	30407	1.81	3.3E-02	6755962	NT	Homo sapiens skeletal muscle LIM-protein 1 (HLI) gene, complete cds
4848	17965	30756	0.88	3.3E-02	AW275996.1	EST_HUMAN	xp40504.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2742799 3'
6570	19630	32896	20.14	3.3E-02	BF245995.1	EST_HUMAN	5011853910F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4073787 5'
6570	19630	32897	20.14	3.3E-02	BF245995.1	EST_HUMAN	5011853910F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4073787 5'
6677	22630	36084	0.71	3.3E-02	BF115821.1	EST_HUMAN	7m82204.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'
6677	22630	36085	0.71	3.3E-02	BF115821.1	EST_HUMAN	7m82204.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'
9779	22720	36174	0.72	3.3E-02	AA488202.1	EST_HUMAN	ad0809.s1 Soares NIHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24, 1D5 (HUMAN);
9779	22720	36175	0.72	3.3E-02	AA488202.1	EST_HUMAN	ad0809.s1 Soares NIHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24, 1D5 (HUMAN);
10864	23884		0.46	3.3E-02	H38109.1	EST_HUMAN	y05111.s1 Soares retina N2B4HR Homo sapiens cDNA clone IMAGE:190989 3'
11485	24368	37845	2.47	3.3E-02	BF891107.1	EST_HUMAN	602247171F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4332497 5'
12425	25163		3.71	3.3E-02	T96545.1	EST_HUMAN	y44911.11 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121101 5'
12547	25270		1.69	3.3E-02	AF286965.1	NT	Mus musculus EIF4H gene, partial cds; LNK1 gene, complete cds; and ELN gene, partial cds
12577	25266		3.04	3.3E-02	M81800.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
132	13237	26108	1.27	3.2E-02	AJ002006.1	NT	Cryptidagis cuticulus gene encoding ileal sodium-dependent bile acid transporter
1128	14171	27122	10.01	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68 allele, complete cds
1128	14171	27123	10.01	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68 allele, complete cds
2127	15144		3.6	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
3151	16208	29122	9.51	3.2E-02	BE597353.1	EST_HUMAN	60144241F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3846727 5'
4245	17275		16.99	3.2E-02	X64768.1	NT	H sapiens RP3 gene (XLRP gene 3)
4801	17818	30712	3.75	3.2E-02	AF114182.1	NT	Saxifraga nidiacea maturase (matK) gene, chloroplast gene encoding chloroplast, protein, partial cds
5303	18306		1.34	3.2E-02	Y08924.1	NT	P falcipterus mRNA for AARP2 protein
5813	18709	31866	1.96	3.2E-02	X68709.1	NT	S.griseocarinum whiG-Stv gene
5813	18709	31867	1.96	3.2E-02	X68709.1	NT	S.griseocarinum whiG-Stv gene

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6673	19730	33006	2.23	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W68.14
6676	19733		30.53	3.2E-02	T89387.1	EST_HUMAN	xl33h12.61 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:110087.3 similar to contains
6763	18817	33097	4.01	3.2E-02	AF173945.1	NT	Alu repetitive element contains LTR1 repetitive element;
8036	20878	34372	0.82	3.2E-02	11424049	NT	Saguius ocellus tissue kallikrein gene, complete cds
8643	21611	35033	2.84	3.2E-02	6880565	NT	Homo sapiens cytochrome P-450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
9233	22259		0.7	3.2E-02	AF109718.1	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9580	22542	35992	1.02	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
9580	22542	35993	1.02	3.2E-02	A1278971.1	EST_HUMAN	qim17b04.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1862063.3'
10417	23339		4.18	3.2E-02	AA719795.1	EST_HUMAN	zgs4b12.61 Soares_pineal_gland_N3-HPG Homo sapiens cDNA clone IMAGE:1862063.3'
10723	23845	37138	0.98	3.2E-02	U69762.1	EST_HUMAN	gbL108441 CYTOCHROME C OXIDASE POLYPEPTIDE II (HUMAN);
12812	25978		1.43	3.2E-02	V00574.1	NT	Meacosa mutata chemokine receptor GCR5 mRNA, complete cds
1285	14300		2.28	3.1E-02	4503419	NT	Human germ line gene homologous to bladder carcinoma oncogene T24 (Gene code c-Ha-ras-1) with four exons
1308	14344	27309	1.87	3.1E-02	P18845	SWISSPROT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1909	14933	27929	1	3.1E-02	6671594	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1991	16012		1.18	3.1E-02	Z50097.1	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5356	18441	31194	1.28	3.1E-02	U78104.1	NT	Drosophila melanogaster mRNA for headcase protein
5434	18538		2.26	3.1E-02	AA278478.1	EST_HUMAN	Human telomerase inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5731	18825	32005	0.81	3.1E-02	BF68742.1	EST_HUMAN	zab1.a6b.1 NCL CGAP CGBT Homo sapiens cDNA clone IMAGE:703858.5'
5803	25845	32078	0.52	3.1E-02	AJ391284.1	NT	602066783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789.5'
10391	23313	38763	2.56	3.1E-02	AF034776.1	NT	Naaseta meningitis DNA for region 2 (flab- and flacC-homologs, unknown genes) and flanking genes, strain FAM18
1627	14690		2.21	3.0E-02	AF187125.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
2590	15591	28608	0.97	3.0E-02	AA402242.1	EST_HUMAN	Phytokeinas minus cytochrome oxidase I gene, partial cds, mitochondrial gene for mitochondrial product
3579	16824	29545	0.91	3.0E-02	M94176.1	NT	z65f03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727263.5'
3668	16709	29624	2.77	3.0E-02	AF247644.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3758	16798		0.96	3.0E-02	AW620223.1	EST_HUMAN	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3969	17069		1.45	3.0E-02	AA364003.1	EST_HUMAN	QV2-STO286-10200-040-a09 ST0286 Homo sapiens cDNA
5002	18102	30977	7.41	3.0E-02	AF281074.1	NT	EST17430 Pineal gland II Homo sapiens cDNA 5' end
5092	18102	30978	7.41	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5485	18597		2.99	3.0E-02	AB046793.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
							Homo sapiens mRNA for KIAA1573 protein, partial cds

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6383	19451	32663	0.58	3.0E-02	N98615.1	EST_HUMAN	2a39a10.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element: TAR1 repetitive element:
6383	19451	32694	0.58	3.0E-02	N98615.1	EST_HUMAN	2a39a10.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element: TAR1 repetitive element:
7097	20182	33305	3.17	3.0E-02	AJ242806.1	NT	Cytosine carboxy mRNA for inducible nitric oxide synthase (NOS gene)
7097	20025	33327	2.8	3.0E-02	BE889948.1	EST_HUMAN	801512208F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913548 5'
7091	20025	33328	2.8	3.0E-02	BE889948.1	EST_HUMAN	801512208F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913548 5'
7274	20009	33310	2.29	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7274	20009	33311	2.29	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7442	20408	33760	1.29	3.0E-02	M88524.1	NT	Human dystrophin gene
7636	20783		0.75	3.0E-02	BF248361.1	EST_HUMAN	801854981F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074549 5'
8463	21432		0.48	3.0E-02	BF679708.1	EST_HUMAN	302154964F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295654 5'
8688	21954	35378	0.74	3.0E-02	BF353889.1	EST_HUMAN	IL5HT0704-280800-108-c04 HT0704 Homo sapiens cDNA
9145	22111		1.82	3.0E-02	AF275654.1	NT	Omlthrichynchus anallus coagulation factor X mRNA, complete cds
10526	23747	37248	1.66	3.0E-02	AE001797.1	NT	Thermolobus maritima section 109 of 136 of the complete genome
11566	24506	38063	2.36	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11667	24874	38470	7.84	3.0E-02	AA483216.1	EST_HUMAN	na8704.at1 NCLCGAP_Kid1 Homo sapiens cDNA clone IMAGE:911283
12529	25960	31316	2.02	3.0E-02	R32019.1	EST_HUMAN	YH8304.1.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:134407 3'
12888	25470		2.06	3.0E-02	AW895565.1	EST_HUMAN	QY4-NN0038-270400-187-R05 NN0038 Homo sapiens cDNA
12908	25954		1.98	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Galactose-4-epimerase beta-1, 4-galactose-4-epimerase mRNA, complete cds
2442	19883	28487	1	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
3005	19063	28982	1.14	2.9E-02	BE565644.1	EST_HUMAN	801339428F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3680895 5'
3005	19063	28983	1.14	2.9E-02	BE565644.1	EST_HUMAN	801339428F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3680895 5'
3573	18618	29540	0.8	2.9E-02	V55204.1	NT	Sheep gene for ultra high-sulphur keratin protein
3950	19390	29805	0.72	2.9E-02	H72805.1	EST_HUMAN	Y0076.0.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:233130 5'
6181	19256	32489	1.13	2.9E-02	AF060221.1	NT	Sus scrofa dioxinobutylase II mRNA, complete cds
6424	19491	32743	7.33	2.9E-02	BF032233.1	EST_HUMAN	801452891F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3856598 5'
7142	20118	33431	0.62	2.9E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (fnbA- and fnbC-homologs, unknown genes) and flanking genes, strain FAM18
7460	20426	33792	10.95	2.9E-02	BE271437.1	EST_HUMAN	801140728F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3048830 5'

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7657	20617	33992	0.67	2.9E-02	D28214.1	EST_HUMAN	HUMNK282 Human epidermal keratinocyte Homo sapiens cDNA clone 282
8169	21107	34506	0.53	2.9E-02	AE003932.1	NT	Xylella fastidiosa, section 78 of 229 of the complete genome
8331	21300	34716	0.83	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlotheimiaella chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
8331	21300	34717	0.83	2.9E-02	AF129278.1	NT	Buchnera aphidicola natural-host Schlotheimiaella chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
10016	22943	36409	2.26	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071289-061-c04 PT0014 Homo sapiens cDNA
10018	22943	36410	2.26	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071289-061-c04 PT0014 Homo sapiens cDNA
10233	23158	37127	0.87	2.9E-02	AW970597.1	EST_HUMAN	EST138706 MAGE resequences, MAGN Homo sapiens cDNA
10710	23632	37127	1.07	2.9E-02	AP0000684.1	NT	Aeropyrum pernix genomic DNA, section 777
11388	18618	29540	1.6	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12331	25670	11388	1.46	2.9E-02	AU135817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE10029632 5'
567	19337	28355	1.93	2.9E-02	AF070153.1	EST_HUMAN	EST1382234 MAGE resequences, MAGK Homo sapiens cDNA
3380	18428	29356	1.27	2.9E-02	AF060663.1	NT	Homo sapiens retinal fascin (FSCN2) gene, exon 2
3380	18428	29356	1.27	2.9E-02	AF060663.1	NT	Homo sapiens retinal fascin (FSCN2) gene, exon 2
4341	17368	17368	0.67	2.9E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5208	18215	31090	3.2	2.9E-02	N87073.1	EST_HUMAN	L2083.F Human fetal heart, Lambda Zap Express Homo sapiens cDNA clone L2083 5' similar to TRNA-QUANINE TRANSGLYCOSYLASE
5294	19299	31622	0.93	2.9E-02	M58493.1	NT	Dengue virus type 2 non-structural protein 1 (NS1) gene, partial cds
5655	19862	31622	10.89	2.9E-02	BE741083.1	EST_HUMAN	Y01694078.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE3948067 5'
6881	20204	33533	1.13	2.9E-02	T78960.1	EST_HUMAN	y421b03.F1 Soares fetal liver spleen cDNA clone IMAGE108855 5'
8671	21639	35083	2.24	2.9E-02	AJ05820.1	NT	Catarractsigne plantigrinum mRNA for homeodomain leucine zipper protein (hb-1)
9371	22336	35786	0.82	2.9E-02	AA380762.1	EST_HUMAN	z39560b.F1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE711468 5'
9593	22925	35974	1.03	2.9E-02	AF187872.1	NT	Cavla porcellus inward-rectifying potassium channel Ki2.1 (KCNJ2) gene, complete cds
9687	22620	36071	0.71	2.9E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
10890	23801	37413	0.42	2.9E-02	BF527244.1	EST_HUMAN	602039477.F2 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE417267 5'
12809	25801	25801	1.6	2.9E-02	AF08966.1	EST_HUMAN	Y1202.F1 Soares fetal liver spleen cDNA clone IMAGE126675 5'
12815	25438	25438	1.57	2.9E-02	X06322.1	NT	Yeast CN31C chromosome III RAHS DNA (right arm transcription hot-spot)
1485	14518	27491	1.07	2.7E-02	U96059.1	NT	Human gerriline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRV1, TRV2, TRV3
3445	16492	29411	1.98	2.7E-02	AL161494.2	EST_HUMAN	TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S1P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2P1, TCRBV7S2A1N4T, TCRBV13S3A1S
4230	17266	30143	2.01	2.7E-02	N47258.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 8
4230	17266	30143	2.01	2.7E-02	N47258.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 8

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4230	17259	30144	2.01	2.7E-02	N47268.1	EST_HUMAN	y68h12.r1 Scores_multiple_sclerosis_2NBHSP Homo sapiens cDNA clone IMAGE:280487.5
5319	18425	31178	0.52	2.7E-02	BF245672.1	EST_HUMAN	60188481F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075.5
5516	18616	31549	1.09	2.7E-02	R12245.1	EST_HUMAN	y33d09.r1 Scores_fetal_liver_spleen_NFLS Homo sapiens cDNA clone IMAGE:126657.5 similar to SP-JC2264 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6005	18088	32288	0.68	2.7E-02	X61670.1	NT	T.aestivum pT120 mRNA for wheat type V ribonin
6887	19167	32379	0.51	2.7E-02	AB04799.1	NT	Oryza sativa mRNA for ascorbate oxidase, partial cds
6754	18908		1.03	2.7E-02	X97680.1	NT	A.bisporus pgkA gene
7269	20004	33304	1.93	2.7E-02	AA93571.1	EST_HUMAN	ch96h03.s1 Scores_fetal_fetus_NB2HF8_gw Homo sapiens cDNA clone IMAGE:1624681.3
8140	21077		0.53	2.7E-02	AK024456.1	NT	Homo sapiens mRNA for FLJ00048 protein, partial cds
8160	21068	34487	0.59	2.7E-02	9256542	NT	Mus musculus G21 protein (G21). mRNA
8687	21665		1.23	2.7E-02	AI377036.1	EST_HUMAN	lc28g08.x1 Scores_fetal_fetus_NB2HF8_gw Homo sapiens cDNA clone IMAGE:2065982.3 similar to contains Alu repetitive element;
573	13642	26556	1.25	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2374	15392	28404	2.54	2.6E-02	AA460021.1	EST_HUMAN	ab02b02.s1 Stratusgene fetal retina 637202 Homo sapiens cDNA clone IMAGE:839565.3
2376	15394	28405	3.05	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (HRC). mRNA
2378	15384	28407	3.05	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (HRC). mRNA
2926	15984		1.52	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G6A, NG22, G6, HSP70, HSP70, HSC70, and smRNP genes, complete cds; GTA gene, partial cds; and unknown genes
3989	17028		0.91	2.6E-02	AW181945.1	EST_HUMAN	Chicken dorsofin-1 mRNA, complete cds
4942	17568	30848	3.25	2.6E-02	L12032.1	NT	Demococcus radiodurans R1 edition 151 of 228 of the complete chromosome 1
5104	18114	30987	1.8	2.6E-02	AE002014.1	NT	Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
5128	18137	31014	3.05	2.6E-02	AW241154.1	EST_HUMAN	xa02b04.x1 NCI_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383.3 similar to SW-Y069_HUMAN
5944	19030		0.6	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
5992	19076		0.65	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6345	19414		6.38	2.6E-02	AI206030.1	EST_HUMAN	qg2771.x1 NCI_CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1762317.3
6565	19525	32890	1.88	2.6E-02	BE621748.1	EST_HUMAN	601483473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895678.3
7001	20127	33441	0.82	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L strain Wyeth
7001	20127	33442	0.82	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L strain Wyeth
7095	20029	33333	6.03	2.6E-02	6881271	NT	Rattus norvegicus Nerve growth factor receptor (as (Ngfr). mRNA
7516	20451	33842	0.85	2.6E-02	P21884	SW/ISSPROT	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)
8860	21617	35237	0.71	2.6E-02	AA860946.1	EST_HUMAN	ak2204.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1406719.3
9715	22743	36164	1.27	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070). mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10072	22999	36468	0.7	2.6E-02	AF114952.1	NT	Saccharomyces cerevisiae NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10072	22999	36468	0.7	2.6E-02	AF114952.1	NT	Saccharomyces cerevisiae NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10769	23669	37196	4.31	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11171	24680		2.02	2.6E-02	AA279951.1	EST_HUMAN	z884c02.t1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:704162.5'
11889	24770	38559	1.61	2.6E-02	AW500547.1	EST_HUMAN	UHLF-BND-alk-e-10-0-UJLT.NH.MGC_50 Homo sapiens cDNA clone IMAGE:3077468.5'
12457	25944	31313	1.96	2.6E-02	BF343827.1	EST_HUMAN	on26f08.y5 NCI CGAP Bm64 Homo sapiens cDNA clone IMAGE:4150944.5'
533	13604	26522	1.85	2.5E-02	A1793130.1	EST_HUMAN	on26f08.y5 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1557827.5'
533	13604	26523	1.85	2.5E-02	A1793130.1	EST_HUMAN	on26f08.y5 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1557827.5'
810	13688	28817	9.19	2.5E-02	BE974314.1	EST_HUMAN	601660305R2 NIH.MGC_83 Homo sapiens cDNA clone IMAGE:3950685.3'
870	13926	28884	6.9	2.5E-02	BE974314.1	EST_HUMAN	601660305R2 NIH.MGC_83 Homo sapiens cDNA clone IMAGE:3950685.3'
2773	15765		2.26	2.5E-02	U12871.1	NT	Rattus norvegicus rapillin-3A mRNA, complete cds
2968	16026	28949	3.43	2.5E-02	X96897.1	NT	H. Lepterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1
2968	16026	28950	3.43	2.5E-02	X96897.1	NT	H. Lepterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1
4075	18316	30005	1.02	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4075	18316	30006	1.02	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4233	17282	30146	6.52	2.5E-02	AW592114.1	EST_HUMAN	H33RH08.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834015.3'
5759	18891	32073	0.65	2.5E-02	A1732776.1	EST_HUMAN	z885c10.x5 Soares, every tumor NIHOT Homo sapiens cDNA clone IMAGE:810354.3'
6317	19388		4.71	2.5E-02	BE670128.1	EST_HUMAN	7c3c0e09.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284008.3' similar to contains L1.1 L1 repetitive element
6334	19403		4.42	2.5E-02	BE740888.1	EST_HUMAN	601578305F1 NIH.MGC_9 Homo sapiens cDNA clone IMAGE:3928054.5'
6470	19535	32783	0.97	2.5E-02	L29029.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7927	20870	34288	1.48	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI CGAP Bm64 Homo sapiens cDNA clone IMAGE:4213406.5'
7927	20870	34259	1.48	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI CGAP Bm64 Homo sapiens cDNA clone IMAGE:4213406.5'
8137	21074	34474	0.54	2.5E-02	AF129458.1	NT	Chlamydomonas reinhardtii class II DNA polymerase (PhiR2) gene, complete cds
9177	22143	35570	0.82	2.5E-02	Q61713	SWISSPROT	CHORDIN PRECURSOR ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
9177	22143	35570	0.82	2.5E-02	Q61713	SWISSPROT	CHORDIN PRECURSOR ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
10426	23346		0.55	2.5E-02	X711303.1	NT	w008c10.x1 NCI CGAP GC68 Homo sapiens cDNA clone IMAGE:2816370.3'
10547	23387	37391	0.67	2.5E-02	A1147615.1	EST_HUMAN	D2 domain
11161	24119	37646	2.15	2.5E-02	Q10335	SWISSPROT	q102z6a8.x1 Soares, pregnant, uterus, NIHPU Homo sapiens cDNA clone IMAGE:1696882.3'
11161	24119	37646	2.15	2.5E-02	Q10335	SWISSPROT	HYPOHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
11161	24119	37647	2.15	2.5E-02	Q10335	SWISSPROT	HYPOHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I



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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11227	24180		3.01	2.5E-02	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IiAlpha) and major histocompatibility protein class II beta chain (IiBeta) genes, complete cds;
12059	24932		1.47	2.5E-02	AB007546.1	NT	Human sapiens gene for LECT2, complete cds
12418	25685		3.35	2.5E-02	11420078	NT	Human sapiens similar to ALEX3 protein (H. sapiens) (LOC358634), mRNA
12568	25751		1.47	2.5E-02	11435220	NT	Human sapiens myogen-activated protein kinase kinase 13 (MAPKK13), mRNA
12696	25953		2.24	2.5E-02	U60169.1	NT	Human sapiens putative protein kinase Mica (Mica) gene, complete cds
12709	25965	31170	3.42	2.5E-02	BE973327.1	EST_HUMAN	D10165236R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE353513 3'
175	13276	26203	0.69	2.4E-02	A1376592.1	EST_HUMAN	tc72607.x1 Soares, NIH/MPU, S1 Homo sapiens cDNA clone IMAGE2070156 3'
1802	14634	27610	2.24	2.4E-02	H65984.1	EST_HUMAN	Y7511.r1 Soares fetal liver spleen 1NF1.S Homo sapiens cDNA clone IMAGE211149 5'
2060	15884	28008	1.73	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2060	15884	28009	1.73	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4398	17424	30308	1.43	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4549	17572	30481	1.43	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5227	18235	30482	1.43	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
6340	19409	32650	0.97	2.4E-02	AL161985.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
6498	19560	32811	0.65	2.4E-02	M31650.1	EST_HUMAN	ZK3304.x1 Soares fetal liver spleen 1NF1.S Homo sapiens cDNA clone IMAGE416791 3'
6498	19560	32812	0.65	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7431	20398	33750	1.38	2.4E-02	Z00573.1	EST_HUMAN	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7448	20414	33767	1.05	2.4E-02	X12825.1	NT	H5A4CACKVX 1, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7448	20414	33768	1.05	2.4E-02	X12825.1	NT	Rat gene for uncoupling protein (UCP)
8158	21097	34495	0.62	2.4E-02	P98092	SWISSPROT	Rat gene for uncoupling protein (UCP)
8159	21097	34496	0.62	2.4E-02	P98092	SWISSPROT	HEMOGUTIN PRECURSOR (HUMORAL LECTIN)
8222	21191		0.57	2.4E-02	AW813007.1	EST_HUMAN	HEMOGUTIN PRECURSOR (HUMORAL LECTIN)
8275	21244		0.58	2.4E-02	M16780.1	NT	RC3-S10186-220300-019-H06 Homo sapiens cDNA
							Human retinotransposon 3' long terminal repeat
8784	21751		0.53	2.4E-02	H76378.1	EST_HUMAN	Y412605.x1 Soares fetal liver spleen 1NF1.S Homo sapiens cDNA clone IMAGE233576 3' similar to contains
							Alu repetitive element/contains A3R repetitive element;
8876	21843	35285	11.43	2.4E-02	N69442.1	EST_HUMAN	g5K0209/RATSR7K Rat (RNA) contains A3R b1 A3R repetitive element;
9338	22303	35731	0.49	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
							z091.c06.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE745354 3' similar to gpJ04422 (SLET
9363	22328	35757	0.81	2.4E-02	AA625660.1	EST_HUMAN	AMYLLOID POLYPEPTIDE PRECURSOR (HUMAN) contains Alu repetitive element/contains element XTR

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe Seq ID NO:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10050	22077	36443	0.46	2.4E-02	AF124160.1	NT	Arabidopsis thaliana methylglutathione synthase sulphydrylase (xms6) gene, complete cds
10050	22077	36444	0.46	2.4E-02	AF124160.1	NT	Arabidopsis thaliana methylglutathione synthase sulphydrylase (xms6) gene, complete cds
10165	23060	36568	2.57	2.4E-02	AF069264.1	EST_HUMAN	AY069264 GKRC Homo sapiens cDNA clone GKDC033.5
10340	23264	36743	2.78	2.4E-02	AA493894.1	EST_HUMAN	h07b12.1 NCJ CGAP_T147 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element
10376	23886		1.35	2.4E-02	BE387111.1	EST_HUMAN	601274622F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615902.5
11900	24781	38398	1.81	2.4E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; amRNP, G7A, NG23, MutS homolog, CLOP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11900	24781	38399	1.81	2.4E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; amRNP, G7A, NG23, MutS homolog, CLOP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
12208	25050		2.39	2.4E-02	6627609	NT	Bacteriophage phi67, complete genome
12393	25152	31855	1.7	2.4E-02	6763835	NT	Mus musculus DnB1 homolog 1 (E. coli) (DnB1), mRNA
12418	25188	31823	3.48	2.4E-02	BE928699.1	EST_HUMAN	MRO-F10175-310800-202-608 FT0175 Homo sapiens cDNA
12474	25222	31791	1.59	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12474	25222	31833	1.59	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12843	26327		7.98	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for non-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
1889	14613		5.26	2.3E-02	U05340.1	EST_HUMAN	z854q08.r1 Soares, fetal lung, NHBL19W Homo sapiens cDNA clone IMAGE:286284.5
1904	14528		8.44	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2358	15066	28398	3.16	2.3E-02	U74263.1	NT	S. cerevisiae chromosome IV reading frame ORF YOL245c
3684	19737	29650	4.2	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH.P, Human foetal Brain Whole tissue Homo sapiens cDNA
4176	17207	30093	0.8	2.3E-02	L24789.1	NT	Gallus gallus connectin 45.6 (Cx45.6) gene, complete cds
4176	17207	30094	0.8	2.3E-02	L24789.1	NT	Gallus gallus connectin 45.6 (Cx45.6) gene, complete cds
4450	17476	30364	1.52	2.3E-02	AF089107.1	EST_HUMAN	GM4-NN0080-290400-180-004 NN0080 Homo sapiens cDNA
4477	17503	30388	0.78	2.3E-02	BE936225.1	EST_HUMAN	CMS-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4477	17503	30398	0.78	2.3E-02	BE936225.1	EST_HUMAN	CMS-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4478	18317	30390	1.23	2.3E-02	AF050593.1	EST_HUMAN	xs25d08.x1 NCJ CGAP_U02 Homo sapiens cDNA clone IMAGE:270871.3
4478	18317	30391	1.23	2.3E-02	AF050593.1	EST_HUMAN	xs25d08.x1 NCJ CGAP_U02 Homo sapiens cDNA clone IMAGE:270871.3
4925	17646	30534	2.89	2.3E-02	BF026487.1	EST_HUMAN	601672276F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3565388.5
4925	17646	30535	2.89	2.3E-02	BF026487.1	EST_HUMAN	601672276F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3565388.5

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5203	18212	31086	1.19	2.3E-02	AF257110.1	NT	Rattus norvegicus glutamine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5203	18212	31087	1.19	2.3E-02	AF257110.1	NT	Rattus norvegicus glutamine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5449	18551	31483	3.35	2.3E-02	U96303.1	NT	Caribacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pcbs) homolog gene, partial cds
6363	19432	32676	0.55	2.3E-02	BF108464.1	EST_HUMAN	60182292R1 NH1_MGC_77 Homo sapiens cDNA clone IMAGE:4042829 3'
6774	19826	33112	4.22	2.3E-02	AL161908.2	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7172	19403	31201	0.84	2.3E-02	BE141475.1	EST_HUMAN	MFO-HT0080-01108-002-c09 HT0080 Homo sapiens cDNA
7655	20653	34016	0.52	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8208	21178	34686	5.65	2.3E-02	U93910.2	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8815	21782	35207	0.87	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8815	21782	35208	0.87	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
9044	22010	35431	0.74	2.3E-02	A085380.1	EST_HUMAN	w07810.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9044	22010	35432	0.74	2.3E-02	A085380.1	EST_HUMAN	w07810.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9493	22457	35897	0.89	2.3E-02	P41996	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
10218	23143	36632	0.77	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10350	23312	36791	1.47	2.3E-02	AE000196.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10360	23312	36792	1.47	2.3E-02	AE000196.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
11135	24066	37624	1.71	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12336	25736		7.89	2.3E-02	BE278331.1	EST_HUMAN	60117958R1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:3546667 5'
12742	25592	31755	1.5	2.3E-02	BF528462.1	EST_HUMAN	60204362R1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12742	25592	31756	1.5	2.3E-02	BF528462.1	EST_HUMAN	60204362R1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12843	25453	31724	3.2	2.3E-02	U93304.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12887	25583		2.48	2.3E-02	U11077.1	NT	Dietysbium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
13100	25533		1.82	2.3E-02	11426388	NT	Homo sapiens dead finger (Drosophila)-like 1 (DRIL1), mRNA
739	13800	26739	4.3	2.2E-02	AF018267.1	NT	Columbia liva nucleotide diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1762	14791		1.59	2.2E-02	4557448	NT	Homo sapiens chromatinin helixase DNA binding protein 2 (CHD2) mRNA
2031	15050	28095	1.68	2.2E-02	Z82001.1	NT	S. pneumoniae pcpA gene and open reading frames
3448	16495		2.16	2.2E-02	AA577785.1	EST_HUMAN	m24604.g1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3660	16703		3.48	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3867	16906	29814	1.26	2.2E-02	AW601317.1	EST_HUMAN	PMO-B10340-170100-004-B03 B10340 Homo sapiens cDNA
3941	16881	29596	0.74	2.2E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL246c

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5105	18115	30698	1.17	2.2E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
7458	20424	33760	3.37	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GK6 Homo sapiens cDNA clone GK6AND03.3'
8714	21882	35100	2.28	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8714	21882	35110	2.28	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9161	22127	35555	0.77	2.2E-02	X79488.1	NT	P. vulgaris eltha tub 2 mRNA
10045	22972	36438	2.26	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10045	22972	36438	2.26	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10565	23487		0.91	2.2E-02	6678140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssar1), mRNA
11540	24481	38033	1.8	2.2E-02	BE797601.1	EST_HUMAN	601584309F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3688571.5'
12802	25504		5.72	2.2E-02	AA503553.1	EST_HUMAN	ne47107.1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:900541.3' similar to contains A1u repetitive element
419	13492		5.37	2.1E-02	AV781502.1	EST_HUMAN	AV781502 MDS Homo sapiens cDNA clone MOSADG01.5'
449	13522		8.77	2.1E-02	AF029728.1	NT	Dicotyledon discoidium histidine kinase C (dhkc) mRNA, complete cds
1268	14303	27264	8.3	2.1E-02	U22073.1	NT	Bacillus subtilis cdkLM cluster, Cdk (cdk), and spore coat protein CdkM (cdm) genes, complete cds
1387	14420	27380	0.99	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1387	14420	27380	0.99	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1787	14828	27611	1.28	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1787	14828	27612	1.26	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1787	14828	27613	1.26	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1980	15001	29004	1.01	2.1E-02	AF100989.1	NT	Tegula aureodentata major acrosomal protein precursor (TMAP) mRNA, complete cds
2050	15069	28099	0.9	2.1E-02	BE072546.1	EST_HUMAN	PW2-B10546-120100-001-f11 B10546 Homo sapiens cDNA
2050	15069	28099	0.9	2.1E-02	BE072546.1	EST_HUMAN	PW2-B10546-120100-001-f11 B10546 Homo sapiens cDNA
2591	15592	28609	1.04	2.1E-02	AA226095.1	EST_HUMAN	nc21g03.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008920
2827	13639	28784	4.45	2.1E-02	N28266.1	EST_HUMAN	yx43107.1 Sceres melanocyte 2N84M Homo sapiens cDNA clone IMAGE:284641.5'
3164	15069	28098	1.02	2.1E-02	BE072546.1	EST_HUMAN	PW2-B10546-120100-001-f11 B10546 Homo sapiens cDNA
3164	15069	28098	1.02	2.1E-02	BE072546.1	EST_HUMAN	PW2-B10546-120100-001-f11 B10546 Homo sapiens cDNA
3957	16942	29861	0.98	2.1E-02	AA619271.1	EST_HUMAN	z483009.1 Sceres, total, fetus, N284F8, 9w Homo sapiens cDNA clone IMAGE:798121.5'
4028	17068	29867	0.97	2.1E-02	BF203457.1	EST_HUMAN	60158080F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4099407.5'
4157	17186	30076	0.64	2.1E-02	Z74263.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL246c
4339	17566	30249	1.4	2.1E-02	BF343655.1	EST_HUMAN	602015308F1 NCI_CGAP_B1064 Homo sapiens cDNA clone IMAGE:4161161.5'
4473	17499	30384	2.15	2.1E-02	U44914.1	NT	Borrelia burgdorferi plesmid gp32.2, e-pC and erpD genes, complete cds; and unknown genes

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4463	17508	30987	1.13	2.1E-02	AI768127.1	EST_HUMAN	wg81d11.x1 Soares_NSF_F8_SW_OT_PA_P31 Homo sapiens cDNA clone IMAGE:2371609 3'
4739	17750	30654	5.69	2.1E-02	Y08501.1	NT	A. Italiana mitochondrial genome, part A
4761	17781	30677	1.5	2.1E-02	AA665737.1	EST_HUMAN	ac55012.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
5256	18264	31133	1.07	2.1E-02	BF028405.1	EST_HUMAN	60167141TF1 NHLMGC_20 Homo sapiens cDNA clone IMAGE:3864410 5'
5723	18817	31988	0.75	2.1E-02	AW379529.1	EST_HUMAN	CM4-H10244-11189-040-R05 HT0244 Homo sapiens cDNA
7268	20003	33303	0.65	2.1E-02	BF086198.1	EST_HUMAN	QY3-GN0058-120900-328-e12 GN0058 Homo sapiens cDNA
8864	21831	35254	0.66	2.1E-02	9750238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9861	22797	36250	0.51	2.1E-02	AA084288.1	EST_HUMAN	an83607.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains repetitive element; contains element MER11 repetitive element
9880	22916	36381	2.63	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9880	22916	36382	2.63	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10343	23267	36746	1.13	2.1E-02	L28324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
10421	23343	36829	0.88	2.1E-02	AA084288.1	EST_HUMAN	an83607.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains repetitive element; contains element MER11 repetitive element
12584	18345	31617	8.95	2.1E-02	Y19213.1	NT	Homo sapiens putative psoriasis pseudogene for hair keratin, exons 2 to 7
12624	25735	31617	1.4	2.1E-02	L34170.1	NT	Human germline UBELL gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
13003	25557	31603	3.5	2.1E-02	AF183913.1	NT	Ascaris suum brasilianae major outer membrane protein OmsA precursor (omsA) gene, complete cds
19	13139	26037	1.39	2.0E-02	BF002832.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3309588 3' similar to contains MER1.3
20	13140	26038	10.76	2.0E-02	AW695665.1	EST_HUMAN	MER1 repetitive element
259	13356	26280	3.29	2.0E-02	6753635	NT	QY4-NN0039-270400-187-R05 NN0039 Homo sapiens cDNA
295	13369	26317	2.85	2.0E-02	AA456538.1	EST_HUMAN	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
789	13855	26805	1.27	2.0E-02	6753635	NT	an15010.t1 Soares_NhMMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
1089	14133	27085	1.03	2.0E-02	AL098805.1	NT	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
1204	14243	27201	0.79	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1204	14243	27202	0.79	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1890	14915	27909	2.08	2.0E-02	8922463	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1890	14915	27910	2.08	2.0E-02	8922463	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2610	15802		4.57	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3095	13139	26037	1.61	2.0E-02	BF002832.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3309588 3' similar to contains MER1.3

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3159	16215		1.83	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sem6b), mRNA
3241	16298		1.8	2.0E-02	AF093583.1	NT	Arabidopsis thaliana C2H2 zinc finger protein ZFP mRNA, complete cds
4032	17070	26971	1.7	2.0E-02	M18095.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5163	18163		0.4	2.0E-02	A1271995.1	EST_HUMAN	q35a03.x1 NCI CGAP K103 Homo sapiens cDNA clone IMAGE:1866078 3'
5175	18184	31061	0.94	2.0E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5718	18812	31991	0.59	2.0E-02	U34778.1	NT	Caenorhabditis elegans sma-2 mRNA, complete cds
6000	19083	32282	0.73	2.0E-02	L35321.2	NT	Dicotyledon discoidium class VII unconventional myosin (myo) gene, complete cds
7789	20751	34126	1.09	2.0E-02	AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
7789	20751	34127	1.09	2.0E-02	AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
10236	23161		1.99	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10728	23848	37141	1.54	2.0E-02	A160242.1	EST_HUMAN	wt7b02.x1 NCI CGAP_K1411 Homo sapiens cDNA clone IMAGE:2298315 3'
11005	23971	37495	1.84	2.0E-02	Z73696.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 93/102
11899	24664	38241	2.26	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
12148	18351	31296	3.03	2.0E-02	AA45538.1	EST_HUMAN	aa15b10.r1 Soares NIH-MPc S1 Homo sapiens cDNA clone IMAGE:013307 5'
12521	15502		1.99	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
13076	25508		3.4	2.0E-02	T80037.1	EST_HUMAN	x246b09.r1 Soares Infant brain 1N18 Homo sapiens cDNA clone IMAGE:24675 5'
684	13756	26888	2.55	1.9E-02	AA572764.1	EST_HUMAN	tn19a07.s1 NCI CGAP_Prl Homo sapiens cDNA clone IMAGE:914196 similar to contains L1, L1 L1 repetitive element;
1619	14652	27628	1.03	1.9E-02	P18488	SW/ISSPROT	EMPTY SPIRALGLES HOMEOTIC PROTEIN
2055	15074	28063	3.04	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2055	15074	28063	3.04	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2514	15517	28540	1.07	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2916	15974	28897	8.5	1.9E-02	AA713855.1	EST_HUMAN	inv04005.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239337 3'
2964	16022	28897	1.46	1.9E-02	AV648659.1	EST_HUMAN	AV648659 GLC Homo sapiens cDNA clone GLCBLH07 3'
3273	16669		0.72	1.9E-02	AB03361.1	NT	Utricularia stipitata mitochondrial gene for cytochrome b, complete cds
3925	16669		1.36	1.9E-02	N32250.1	EST_HUMAN	x246b02.s1 Soares, multiple, cell cycle, 2N6HWSVP Homo sapiens cDNA clone IMAGE:284331 3'
3718	16761		8.23	1.9E-02	BE739888.1	EST_HUMAN	601872582.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:369564 5'
							element;
3727	16769	29881	0.89	1.9E-02	AI301183.1	EST_HUMAN	tn9a407.x1 NCI CGAP_Lus Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element;
4077	17112	30008	1.59	1.9E-02	AF141940.1	NT	Myoelasma imitans VHA1 precursor (VHA1) and VHA2 precursor (VHA2) genes, partial cds
4222	17251	30137	1.82	1.9E-02	P09081	SW/ISSPROT	HOMEOTIC PROTEIN (PRD-4)
4222	17251	30138	1.82	1.9E-02	P09081	SW/ISSPROT	HOMEOTIC PROTEIN (PRD-4)

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4572	17564	30488	3.65	1.9E-02	A1452986.1	EST_HUMAN	h46d04.x1 Soares, NSF, FB, 9W, OT, PA, P, S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element.
5488	15517	28540	2.88	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5389	18462	31369	0.91	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TOR gamma 1 and gamma 3 gene clusters
5544	18471	31381	1.25	1.9E-02	L47572.1	NT	Meleagris gallopavo paracoxase-2 (PON2) mRNA, complete cds
5895	18974		1.24	1.9E-02	AB019507.1	NT	Drosophila Kanelak gene for glyceral-3-phosphate dehydrogenase, complete cds
7308	20279	33617	1.34	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7308	20279	33618	1.34	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8817	21893		1.2	1.9E-02	AL162754.2	NT	Nesheria meningitidis serogroup A strain Z2491 complete genome, segment 3/7
9685	22639	36096	0.78	1.9E-02	BF316129.1	EST_HUMAN	601866130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
10071	23268	36467	0.43	1.9E-02	L10114.1	NT	Nicotiana tabacum Type I phytochrome (phv5) gene, complete cds
10403	23327	36811	1.09	1.9E-02	BF695832.1	EST_HUMAN	601852285F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076239 5'
10510	23432	36929	0.46	1.9E-02	N039160.1	EST_HUMAN	Y46H08.st Soares, multiple_sclerosis_ZNFHSP Homo sapiens cDNA clone IMAGE:276839 3'
10614	23536	37034	0.5	1.9E-02	D64001.1	NT	Synechocystis sp. PCC6803 complete genome, 20127, 2539000-2844794
12372	25742	31620	3.14	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament gliadin mRNA, complete cds
13026	25574	31696	1.4	1.9E-02	X68271.1	NT	H. sapiens ALIC18 gene exon 16
346	13435	26357	1.35	1.9E-02	AW771104.1	EST_HUMAN	h46d04.x1 NCL CGAP_Cot17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element.
686	13749	26675	1.39	1.9E-02	BF308122.1	EST_HUMAN	601804329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139583 5'
1164	14203	27159	1.87	1.9E-02	X17684.1	NT	H.francisci mRNA for myelin basic protein (MBP)
2687	15693	28701	1.78	1.9E-02	AE005444.1	NT	Pseudomonas aeruginosa PAO1, section 105 of 529 of the complete genome
3224	16279		1.08	1.9E-02	AB05628.1	EST_HUMAN	h46d04.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:2090295 3'
3802	16842	29853	1.01	1.9E-02	AW876122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3902	16942	29854	1.01	1.9E-02	AW876122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4113	17147		1.04	1.9E-02	AA861446.1	EST_HUMAN	sk24104.st Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4461	17487	30374	1.49	1.9E-02	AW693683.1	EST_HUMAN	QV4-DT0021-301296-071-b11 DT0021 Homo sapiens cDNA
4592	18007	30695	0.98	1.9E-02	CC08010	SWISSPROT	HYPOTHETICAL PROTEIN D845024.2
5287	18263	31154	0.98	1.9E-02	AF25571.1	NT	Oriza sativa putative histone deacetylase HD2 mRNA, complete cds
6524	19537	32845	0.59	1.9E-02	AE002518.1	NT	Nesheria meningitidis serogroup B strain MC58 section 180 of 200 of the complete genome
6524	19537	32845	0.59	1.9E-02	AE002518.1	NT	Nesheria meningitidis serogroup B strain MC58 section 190 of 200 of the complete genome
6882	20205	33534	4.59	1.9E-02	PI4310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
7689	20657	34021	0.65	1.9E-02	BF125680.1	EST_HUMAN	601762268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
7722	20657	34021	0.98	1.9E-02	BF125680.1	EST_HUMAN	601762268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
8467	21436	34854	0.77	1.9E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8811	21778	35203	0.79	1.8E-02	AW905327.1	EST_HUMAN	QV2-NN1073-220400-158-h99 NN1073 Homo sapiens cDNA
8857	21824	35247	0.75	1.8E-02	6678943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9848	22785	36238	0.5	1.8E-02	BF241924.1	EST_HUMAN	601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9849	22785	36239	0.5	1.8E-02	BF241924.1	EST_HUMAN	601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
10000	22927		2.03	1.8E-02	AA897543.1	EST_HUMAN	g6208.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb:11672 ZINC FINGER PROTEIN 91 (HUMAN);
10423	23345	36830	1.35	1.8E-02	BE778274.1	EST_HUMAN	601483548F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866983 5'
10686	23508	37000	1.2	1.8E-02	X98833.1	NT	L1 tagonella mRNA for myomodulin neuropeptide precursor
11765	23920	37436	1.7	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11765	23920	37439	1.7	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11835	24816	38413	2.73	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (87)
11848	24827	38422	3.16	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
13105	25026	31680	1.35	1.8E-02	R40255.1	EST_HUMAN	y80401.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28986 3' similar to gb:M62783
13105	25626	31681	1.35	1.8E-02	R40255.1	EST_HUMAN	ALPHA-N-ACETYLGLACTOSAMINIDASE PRECURSOR (HUMAN);
907	13952	26918	0.8	1.7E-02	BE394869.1	EST_HUMAN	y80d01.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28985 3' similar to gb:M62783
						EST_HUMAN	ALPHA-N-ACETYLGLACTOSAMINIDASE PRECURSOR (HUMAN);
						EST_HUMAN	601310628F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3932190 5'
1806	14834	27823	2.15	1.7E-02	AV673183.1	EST_HUMAN	H33403.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2633740 3' similar to contains L1.11 L1 repetitive element 1;
						EST_HUMAN	H33403.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2633740 3' similar to contains L1.11 L1 repetitive element 1;
1808	14834	27824	2.15	1.7E-02	AW57183.1	EST_HUMAN	H33403.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2633740 3' similar to contains L1.11 L1 repetitive element 1;
1887	14912		4.23	1.7E-02	AL63204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2121	15138		11.19	1.7E-02	AB004816.1	NT	Oryzopsis eulalioides mRNA for mltgugm128, complete cds
2301	15313	28333	1.03	1.7E-02	S74186.1	NT	Intersatellite INRA41 (Ovis aries)-sheep, Genomic, 381 nt, segment 1 of 2
2648	15645		1.18	1.7E-02	7657495	EST_HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX6), mRNA
3011	16069	28690	0.96	1.7E-02	AI147615.1	EST_HUMAN	qb22608.x1 Soares_pregnant_uterus_NHHPU Homo sapiens cDNA clone IMAGE:1696982 3'
						EST_HUMAN	HM45404.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element 1;
3523	16569		5.62	1.7E-02	AW827958.1	EST_HUMAN	ac16954.s1 Strategene ovary (H37217) Homo sapiens cDNA clone IMAGE:566927 3' similar to contains Alu repetitive element; contains element MER2a repetitive element 1;
4198	17229		0.96	1.7E-02	AA686818.1	EST_HUMAN	y68608.r1 Soares fetal liver ap1en 1N1FS Homo sapiens cDNA clone IMAGE:124647 5'
4228	17267		2.04	1.7E-02	R02506.1	EST_HUMAN	qm08407.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4482	17507	30396	0.7	1.7E-02	AI305279.1	EST_HUMAN	FINGER PROTEIN 30 (HUMAN);



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4857	17980	30471	1.92	1.7E-02	AW673183.1	EST_HUMAN	H34403.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2863740 3' similar to contains L1/L1 repetitive element;
4744	17764	30658	1.54	1.7E-02	V00841.1	NT	Messenger RNA for anglerfish ( <i>Lophius americanus</i> ) somatostatin II
4851	17868		7.05	1.7E-02	A015076.1	EST_HUMAN	057402.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1940858 3'
5105	18116	30989	0.74	1.7E-02	6881283	NT	Rattus norvegicus N-arginine diase convertase 1 (Nrd1), mRNA
5229	18237		0.91	1.7E-02	AJ229041.1	NT	Homo sapiens 989 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 contains Alu repetitive element;
5248	19321	32551	1.53	1.7E-02	AI769247.1	EST_HUMAN	wg35f09.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387113 3' similar to contains Alu repetitive element;
6618	19676		0.64	1.7E-02	Z28383.1	NT	T.niveum (ATCC34921) simA gene for cyclosporine synthetase
6731	19787	33085	1.37	1.7E-02	A038280.1	EST_HUMAN	cy65f03.x1 Soares, fetal_liver, spleen, 1NfLS_S1 Homo sapiens cDNA clone IMAGE:1872661 3'
7251	19886	33284	1.31	1.7E-02	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7411	20378	33726	1.95	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
7581	20543	33502	0.85	1.7E-02	L07889.1	NT	Human apolipoprotein (a) gene, exon 1
7591	20543	33903	0.85	1.7E-02	L07889.1	NT	Human apolipoprotein (a) gene, exon 1
8016	20554		1.98	1.7E-02	AJ010770.1	NT	Homo sapiens hypoxanthine gene, exons 1-50
9791	21114	34514	0.91	1.7E-02	U21854.1	NT	Caenorhabditis elegans cGAP1 protein gene, complete cds
10057	22884	36453	1.31	1.7E-02	AL040554.1	EST_HUMAN	DKFZP494I0314_r1 434 (synonym: hlec3) Homo sapiens cDNA clone DKFZP494I0314 5'
12084	24856	38551	1.59	1.7E-02	5902007	NT	Homo sapiens serum constituent protein (MSE55), mRNA
12910	25910	31424	3.15	1.7E-02	AW693482.1	EST_HUMAN	GMA-HN1030-940400-130-06 NNT1030 Homo sapiens cDNA
13059	25958	31687	1.31	1.7E-02	AA846926.1	EST_HUMAN	oe08d04.x1 NCL_CGAP_O22 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSR1 repetitive element;
512	13593		2.22	1.6E-02	ALC21929.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 13/162
1655	14697	27673	0.91	1.6E-02	Y18899.1	NT	Tropomyosin alpha3, flab3 and flid genes for flagellin subunit proteins and CAP protein homologue
2572	15573	28593	0.95	1.6E-02	AJ005345.1	NT	hmd1d05.s1 NCL_CGAP_Ewt Homo sapiens cDNA clone IMAGE:910687
2851	15948	28671	1.45	1.6E-02	AA484872.1	EST_HUMAN	hmd1d05.s1 NCL_CGAP_Ewt Homo sapiens cDNA clone IMAGE:910687
2704	15700		1.37	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
3537	16593	29506	4.46	1.6E-02	AW650632.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28
4204	17235		2.14	1.6E-02	AF10520.1	NT	KIFC1, F-actin-binding protein, BING1, tapasin, RAGS-like, KE2, BIN4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Secm21 gene, partial>
4329	17957	30245	0.86	1.6E-02	AW875407.1	EST_HUMAN	QVZ-PT0012-140100-930-107 PT0012 Homo sapiens cDNA
5172	18181		0.76	1.6E-02	N80156.1	EST_HUMAN	zaf5e067.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:287444 3'
5325	18431	31183	0.49	1.6E-02	AL281385.1	EST_HUMAN	qu42b09.x1 NCL_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1987417 3'

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6705	18800	31977	1.33	1.6E-02	8671716	NT	Mus musculus CD5 antigen (Cd5), mRNA
6798	19853	33138	2.07	1.6E-02	AB015281.1	NT	Candida albicans CAGCR3 gene, complete cds
7117	20091	33354	0.93	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7117	20091	33355	0.93	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7678	20917	34308	1.08	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8458	21427	34844	0.72	1.6E-02	AJ277682.1	NT	Human septins peritub gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8519	21487		1.5	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
10400	23322		1.98	1.6E-02	AF078764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10785	23706	37206	1.2	1.6E-02	AA572818.1	EST_HUMAN	Human septins cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
10785	23706	37207	1.2	1.6E-02	AA572818.1	EST_HUMAN	Human septins cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
11255	25705	37730	1.83	1.6E-02	Z94828.1	NT	G. gallus microsatellite DNA (LE0280 (=T7611E11))
11547	24488	38042	1.7	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11547	24488	38043	1.7	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11839	24722	38307	1.66	1.6E-02	AI373598.1	EST_HUMAN	q26e10.x1 Soares, pregnant, uterus, NB-IPU Homo sapiens cDNA clone IMAGE:2042442 3'
12347	18334	31172	1.39	1.6E-02	Q84176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
12347	18334	31173	1.39	1.6E-02	Q84176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
752	13813		20.75	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2162	15168	28184	4.44	1.5E-02	N39521.1	EST_HUMAN	y27D07.51 Soares fetal liver apolip N1FLS Homo sapiens cDNA clone IMAGE:245925 3'
2185	15200	28220	1.82	1.5E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3074	18131	29043	2.54	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3074	18131	29044	2.54	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3737	18779	29692	1.06	1.5E-02	BF062942.1	EST_HUMAN	MR4-TN0115-080900-201-412 TN0115 Homo sapiens cDNA
6426	19483	32745	1.33	1.5E-02	Q03711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7541	20504		1.59	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
7631	20561	33584	1.38	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8206	21162	34585	1.5	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8213	21178	34593	4.62	1.5E-02	11417739	NT	Homo sapiens valyl-RNA synthetase 2 (VARS2), mRNA
9182	22146	35575	0.93	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NC1 CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4154504 5'
9629	22812	36266	0.58	1.5E-02	AF068774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9629	22812	36266	1.58	1.5E-02	D44806.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
10170	23095	36574	0.95	1.5E-02	R32667.1	EST_HUMAN	yH4b10.1 Soares placenta N2b2P Homo sapiens cDNA clone IMAGE:133531 5'

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10170	23095	36575	0.95	1.5E-02	R32667.1	EST_HUMAN	h54510.r1 Source placenta Nb2-IP Homo sapiens cDNA clone IMAGE:133531.5
11503	24445	37997	2.75	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCB3) variant-specific surface protein (var-2, var-3) genes, complete cds's
11537	24478	38028	2.92	1.5E-02	AL111238.1	NT	Babesia chinea strain 14 cDNA library under conditions of nitrogen deprivation
12564	25783		2.04	1.5E-02	AW760834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
13078	25610		1.3	1.5E-02	AI763127.1	EST_HUMAN	w08h03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389493.3 similar to contains Alu repetitive element; contains element MER26 MSR1 repetitive element.
417	13460		1.99	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 64 of the complete genome
1120	14164	27115	5.44	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC81225), mRNA
1261	14266		1.74	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1301	14337		3.4	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (XNGNR1b) mRNA, complete cds
1520	14562		1.03	1.4E-02	AV723765.1	EST_HUMAN	AV723765 HTB Homo sapiens cDNA clone HTBA4111.5
3226	16281	26204	2.04	1.4E-02	AF160969.2	NT	Brifobacterium longum Na <sup>+</sup> /H <sup>+</sup> antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xyR) gene, partial cds
3409	16458	29390	0.98	1.4E-02	AW074212.1	EST_HUMAN	x08009.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2675793.3
3496	16543	29487	6.29	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3495	16543	29498	6.29	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3569	16712	29627	6.69	1.4E-02	6969918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4516	17541	30427	6.1	1.4E-02	AW962688.1	EST_HUMAN	EST1374761 MAGC resources, MAGC Homo sapiens cDNA
4516	17541	30428	6.1	1.4E-02	AW962688.1	EST_HUMAN	EST1374761 MAGC resources, MAGC Homo sapiens cDNA
4911	17928	30818	8.08	1.4E-02	BE793142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280.5
4911	17928	30819	8.08	1.4E-02	BE793142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280.5
5130	18139	31017	1.01	1.4E-02	AW948463.1	EST_HUMAN	CMO-FN0041-120600-370-H09 FN0041 Homo sapiens cDNA
5888	25992		0.95	1.4E-02	X91338.1	NT	H. sapiens LaSS-B pseudogene 3
6555	19615	32680	4.9	1.4E-02	AA559030.1	EST_HUMAN	n111d04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029960.3 similar to contains Alu repetitive element
6555	19615	32681	4.9	1.4E-02	AA559030.1	EST_HUMAN	n111d04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029960.3 similar to contains Alu repetitive element
8478	21447		1.61	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 881/162
9249	22215	35645	0.77	1.4E-02	M81702.1	NT	Candida badoili methylglutathione oxidase (AOD1) gene, complete cds
9510	22473	35917	0.9	1.4E-02	AL272665.1	NT	Homo sapiens SP2 gene for secreted phosphoprotein 24 precursor, exon 1-8
9755	22696	36153	2.15	1.4E-02	BE544561.1	EST_HUMAN	601078206F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241.5
10623	23943		0.98	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12254	25080	38172	2.14	1.4E-02	X80458.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12616	25312		1.47	1.4E-02	AF324983.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12682	25474		1.96	1.4E-02	11426868	NT	Human sapiens sperm associated antigen 7 (SPAG7), mRNA
19172	14983	27894	2.05	1.3E-02	AL163201.2	NT	Human sapiens chromosome 21 segment HS21C001
3227	18282	28206	2.31	1.3E-02	BF687081.1	EST_HUMAN	602128475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3227	18282	28206	2.31	1.3E-02	BF687081.1	EST_HUMAN	602128475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3953	17033		1.38	1.3E-02	AF108288.1	NT	Mus musculus beta-actin gene, complete cds
							Human gamma T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV35S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBD1, TCRBV1S1, TCRBV1S2>
5317	18423	31225	1.79	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB: X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, nmox28orf
5317	18423	31226	1.79	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB: X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, nmox28orf
6288	19380	32587	1.21	1.3E-02	U80017.1	NT	Human sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
6322	19393	32634	0.7	1.3E-02	M62962.1	NT	C-reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7154	18396	31228	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7154	18396	31229	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7629	20777	34155	4.86	1.3E-02	AI031593.1	EST_HUMAN	ov06050.x1 Soares_papathroid_jumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
8826	21793	35216	1.48	1.3E-02	AF15891.1	NT	Human sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10567	23489	36981	2.18	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10641	23563	37059	0.63	1.3E-02	AE001304.1	NT	Chlamydia trachomatis sactin 31 of 87 of the complete genome
10688	23908	37421	0.44	1.3E-02	AA707741.1	EST_HUMAN	2828a07.61 Soares_prenal_gland_NbHPG Homo sapiens cDNA clone IMAGE:412880 3'
11336	24286	37809	3.74	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S11 Homo sapiens cDNA clone IMAGE:2815036 3'
11336	24286	37810	3.74	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S11 Homo sapiens cDNA clone IMAGE:2815036 3'
12622	25923		1.4	1.3E-02	Z89117.1	NT	Brucella subtilis complete genome (section 14 of 21); from 2589451 to 2812870
12714	25916		2.51	1.3E-02	9653068	NT	Human herpesvirus 6B, complete genome
12866	25716		10.88	1.3E-02	AF152238.1	NT	Human sapiens V1b vasopressin receptor (VPR3) gene, complete cds
214	13314		0.67	1.2E-02	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
355	13443	28308	4.67	1.2E-02	AA050269.1	EST_HUMAN	zif59p1.1 Scores retina N264HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1.1 repetitive element;
453	13528	28456	1.81	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL T71 K10 PROTEIN IN PURS 3 REGION
740	13801	28740	3.32	1.2E-02	AI183522.1	EST_HUMAN	qdb6e12.x1 Scores testis NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.1 L1 repetitive element;
1502	15002	28222	1.82	1.2E-02	AI183213.2	NT	Homo sapiens chromosome 21 segment HS21O013
2160	15205	28225	1.44	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2449	15454	28476	1.65	1.2E-02	AW172350.1	EST_HUMAN	X37609.x1 Scores NF1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2656432 3'
2505	15508	28534	0.99	1.2E-02	BE638310.1	EST_HUMAN	601069406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2505	15508	28535	0.99	1.2E-02	BE638310.1	EST_HUMAN	601069406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2643	15454	28476	1.31	1.2E-02	AW172350.1	EST_HUMAN	X37609.x1 Scores NF1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2656432 3'
3118	16175	28273	6.98	1.2E-02	AA075418.1	EST_HUMAN	Zn88403.r1 Strabagene ovarian cancer (89377219) Homo sapiens cDNA clone IMAGE:545026 5'
3501	16354	28273	2.62	1.2E-02	R62806.1	EST_HUMAN	WT1b08.s1 Scores placenta N62HP Homo sapiens cDNA clone IMAGE:138803 3'
4917	17934	30826	8.36	1.2E-02	6754367	NT	Mus musculus interferon regulatory factor 5 (Irf5), mRNA
4953	17968	30858	1.66	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5080	18090	31008	1.34	1.2E-02	AB019786.1	NT	Cryptos pyrimogaster CpUbiq.T mRNA, partial cds
5121	18131	31008	2.09	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5259	18287	31135	1.01	1.2E-02	AF165576.1	NT	Mus musculus POZ/zinc finger transcription factor ODA-8 mRNA, complete cds
5769	18861	31135	0.5	1.2E-02	AA756018.1	EST_HUMAN	el28f10.x1 Scores testis NHT Homo sapiens cDNA clone 1344235 3'
5946	18926	32120	1.72	1.2E-02	D78589.1	NT	Rana rugosa mRNA for calreticulin, complete cds
6238	19311	32543	0.98	1.2E-02	AF045556.1	NT	Homo sapiens wbcst1 (WBCS1) and wbcst5 (WBCS5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7203	20227	33560	5.57	1.2E-02	AF175412.1	NT	X34412.s1 Scores placenta N62HP Homo sapiens cDNA clone IMAGE:150696 3'
7510	20475	33836	1.07	1.2E-02	H02167.1	EST_HUMAN	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7534	20497	33858	8.5	1.2E-02	AV732893.1	EST_HUMAN	AV732893 HTF Homo sapiens cDNA clone HTFBUC09 5'
7805	20755	34131	0.54	1.2E-02	BF216650.1	EST_HUMAN	601069406F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086253 5'
8330	21269	34715	2.28	1.2E-02	Q11205	SWISSPROT	GMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE-ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GALNAOS) (GAL-BETA-1,3-GALNA-C-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT*4B)
8534	21502	34919	1.31	1.2E-02	AF165612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8534	21502	34920	1.31	1.2E-02	AF165612.1	NT	Homo sapiens fringe protein mRNA, partial cds
9242	22209	176987.1	1.1	1.2E-02	T76987.1	EST_HUMAN	WT2008.s1 Scores fetal liver spleen TNF.LS Homo sapiens cDNA clone IMAGE:113774 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9997	22924	36369	2.63	1.2E-02	AB031013.1	NT	Norwalk-like virus genome 2 gene for capsid protein, complete cds
10030	22957	36425	1.29	1.2E-02	AJ246603.1	NT	Homo sapiens Spast gene for spastin protein
12310	25118	31841	2.74	1.2E-02	U16634	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGU1) (HPER)
12896	25492		5.61	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN-557G06 5'
1274	14309	27270	1.14	1.1E-02	AA070364.1	EST_HUMAN	znf891.1 s1 Stratiogene neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:330924 3'
1719	14749	27734	1.8	1.1E-02	X75491.1	NT	H sapiens LIPA gene, exon 4
1719	14749	27735	1.8	1.1E-02	X75491.1	NT	H sapiens LIPA gene, exon 4
2054	15073	28092	4.08	1.1E-02	BF345263.1	EST_HUMAN	502018037F1 NCJ_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4153808 5'
2889	15948		3.91	1.1E-02	N99523.1	EST_HUMAN	za40e05.1 Scores fetal liver spleen TNF.LS Homo sapiens cDNA clone IMAGE:265040 5'
3535	15581	28505	2.75	1.1E-02	AI653508.1	EST_HUMAN	1995101x1 NCJ_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN
4051	17088		1.52	1.1E-02	BE144837.1	EST_HUMAN	PQ3-HIT0175-300669-001-106 HT0175 Homo sapiens cDNA
4133	17165		0.71	1.1E-02	AW613796.1	EST_HUMAN	Q22889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4867	17894	30772	2.22	1.1E-02	AL046383.2	EST_HUMAN	RCF-ST0187-120200-015-g11 ST0187 Homo sapiens cDNA
							DKFZ586E0924_s1 586 (synonym: hules) Homo sapiens cDNA clone DKFZ586E0924
6272	18345	32578	1.02	1.1E-02	U66480.1	NT	Bacillus subtilis SpoVK (spoVK) YnfA (ynbA) YnfB (ynbB) GlnR (glnR) glutamine synthetase (glnA) (ynhH), YnfI (ynal), YnfJ (ynad), xylan beta-1,4-xylosyl
7855	20800	34176	2.47	1.1E-02	BE149611.1	EST_HUMAN	YnfA (ynbA), YnfB (ynbB), YnfC (ynbC), YnfD (ynbD), YnfE (ynbE), YnfF (ynbF), YnfG (ynbG), YnfH
8105	21042	34441	3.79	1.1E-02	9631284	NT	RC1-HT0256-100300-016-H07 HT0256 Homo sapiens cDNA
8687	21953	35377	0.7	1.1E-02	AW566160.1	EST_HUMAN	Melanoplus sanguinipes entomopoxvirus, complete genome
9174	22140	35566	0.68	1.1E-02	CO4803.1	EST_HUMAN	CKFZ-BN0045-220300-128-102 BN0045 Homo sapiens cDNA
9253	22419	39550	7.21	1.1E-02	Q61982	SWISSPROT	CO4803 Human heart cDNA (Ynkakura) Homo sapiens cDNA clone 3NH4C4040
10289	23214	39698	2.1	1.1E-02	AA082578.1	EST_HUMAN	CD803 LOCUS NOTCH 3 PROTEIN
10454	23376	39869	3.79	1.1E-02	AA314665.1	EST_HUMAN	zn24e01.1 Stratiogene neuroepithelium NT2FRAM 937234 Homo sapiens cDNA clone IMAGE:548328 5'
11324	24274	37802	2.01	1.1E-02	11435505	NT	EST188464 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
12194	25039		3.52	1.1E-02	AA68239.1	EST_HUMAN	Homo sapiens T-box 5 (TBOX5) mRNA
12960	17165		1.67	1.1E-02	AW613796.1	EST_HUMAN	cd7711.1 s1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
7	13127	26027	6.08	1.0E-02	AW646120.1	EST_HUMAN	Alu repetitive element
1526	14559	27530	1.07	1.0E-02	AW386128.1	EST_HUMAN	MR3-ST0176-111089-003-010 CT0176 Homo sapiens cDNA
2578	15579		1.26	1.0E-02	AA806369.1	EST_HUMAN	CM2-HT0177-041099-017-112 HT0177 Homo sapiens cDNA
3108	18163	28075	2.7	1.0E-02	BE35556.1	EST_HUMAN	CO22908.61 NCJ_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1350495 3'
3276	18330	28251	1.33	1.0E-02	BE98996.1	EST_HUMAN	RCO-FN0025-250500-021-002 FN0025 Homo sapiens cDNA
							601946967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3520	16556			1.0E-02	AW845621.1	EST_HUMAN	MRO-CT0060-081069-003-110 CT0060 Homo sapiens cDNA
3395	16935	28845	0.75	1.0E-02	A1065086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
3911	16951	28862	1.06	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21G102
4811	17828	30725	4.97	1.0E-02	6753527	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4881	17898	30787	5.01	1.0E-02	R96967.1	EST_HUMAN	y34301.r1 Soares fetal liver spleen 1NF3S Homo sapiens cDNA clone IMAGE:196633 5'
5036	18049	30929	0.63	1.0E-02	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5490	18590	31501	0.86	1.0E-02	H52681.1	EST_HUMAN	y438111.r1 Soares ovary tumor N3HOT Homo sapiens cDNA clone IMAGE:235941 5'
5940	18830	32114	0.82	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6237	19310	32542	1.02	1.0E-02	AF257303.1	NT	Mus musculus synaptobrevin II (Syx2) gene, complete cds
6305	19376	32614	2.49	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-H01 BT0356 Homo sapiens cDNA
6305	19376	32615	2.49	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-H01 BT0356 Homo sapiens cDNA
6926	20150	33470	2.15	1.0E-02	Z29642.1	NT	Z.mays U3snRNA pseudogene
8748	22689	36145	4.19	1.0E-02	BF036331.1	EST_HUMAN	601439570F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:3863177 5'
8748	22689	36146	4.19	1.0E-02	BF036331.1	EST_HUMAN	601439570F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:3863177 5'
11594	24532		1.96	1.0E-02	AF157559.1	NT	CitRidia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds, mitochondrial gene for mitochondrial product
11895	24660	38238	2.05	1.0E-02	AF160016.1	EST_HUMAN	AV160016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12091	24962		1.47	1.0E-02	AL163262.2	NT	Homo sapiens chromosome 21 segment HS21G082
12276	25990		1.99	1.0E-02	C62203	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A68)
12337	25757	31518	3.9	1.0E-02	AW68521.1	EST_HUMAN	RC2-DT0007-120200-016-H02 DT0007 Homo sapiens cDNA
12358	25816		5.66	1.0E-02	S70330.1	NT	Homo sapiens renal c-peptidase (RDP) gene, complete cds
12722	25789		2.07	1.0E-02	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12873	25873		4.76	1.0E-02	X22854.1	NT	H.sapiens gene for Me491/CD83 antigen
13094	25920	31676	1.7	1.0E-02	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
894	13949	26907	1.77	9.0E-03	A17961.26.1	EST_HUMAN	WH4206.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2883433 3' similar to contains element MER22 MER22 repetitive element
1269	14304		1.88	9.0E-03	BE181869.1	EST_HUMAN	WH4206.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3873346 5'
1476	14510	27485	0.97	9.0E-03	AE001270.1	NT	Troponeura pallidus section 86 of 87 of the complete genome
2405	15412	28436	2.87	9.0E-03	AL161659.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2413	15420	28444	0.95	9.0E-03	AF096934.1	NT	Mus musculus MHC class III protein RPI1 (Rpi1) mRNA, partial cds
2917	15975	28898	0.99	9.0E-03	AJ125174.1	EST_HUMAN	q96099.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1854281 3'
2917	15975	28899	0.99	9.0E-03	AJ125174.1	EST_HUMAN	q96099.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3682	16725	29638	0.87	9.0E-03	J05184.1	NT	S.acidocalcarius thermopsis gene, complete cds
5061	18071	30950	1.01	9.0E-03	T70044.1	EST_HUMAN	y617508.s1 Stratagene lung (4637210) Homo sapiens cDNA clone IMAGE:80919 3'

Table 4

## Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5061	18071	30851	1.01	9.0E-03	T70044.1	EST_HUMAN	yt17b08.s1 Striatagene lung (4637210) Homo sapiens cDNA clone IMAGE:50919 3'
5260	18269	31136	0.95	9.0E-03	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Crhr2), mRNA
5908	18694		1.2	9.0E-03	AI809702.1	EST_HUMAN	wf1704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2381831 3'
6785	19940		4	9.0E-03	BE745968.1	EST_HUMAN	60157438F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:3834752 5'
7698	20553	34020	0.83	9.0E-03	AI242219.1	EST_HUMAN	q87612.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:183974 3'
7712	20569	34036	0.81	9.0E-03	8822570	NT	Homo sapiens histone H1.434 (synonym: h1a3) Homo sapiens cDNA clone DKFZp434L0412 5'
8207	21177		0.99	9.0E-03	AL036991.1	EST_HUMAN	DKFZp434L0412.1 434 (synonym: h1a3) Homo sapiens cDNA clone DKFZp434L0412 5'
8592	21560		0.55	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10221	23146	36635	1.42	9.0E-03	AF223391.1	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
11531	24281		1.8	9.0E-03	P23808	NT	Homo sapiens NF2 gene
12690	25985		2.12	9.0E-03	BE348385.1	EST_HUMAN	hvt7b09.x1 NCL_GAGP_Lu24 Homo sapiens cDNA clone IMAGE:3183181 3'
12989	25549		15.47	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0432 Homo sapiens cDNA
502	13574		3.01	8.0E-03	AA723007.1	EST_HUMAN	z130e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:113506 3' similar to contains Alu repetitive element
891	14043	28697	19.52	8.0E-03	AF106566.1	NT	Homo sapiens edénylosuccinate lyase gene, complete cds
2168	15182	28202	1.86	8.0E-03	AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C083
3321	16372	28293	1.12	8.0E-03	BE171223.1	EST_HUMAN	RC1-HT0545-120200-071-b09 HT0545 Homo sapiens cDNA
3370	18420	28345	0.83	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3689	18732	28644	1.25	8.0E-03	P32844	SWISSPROT	HYPOHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3689	18732	28644	1.25	8.0E-03	P32844	SWISSPROT	HYPOHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4285	17914	30193	1.08	8.0E-03	BE840049.1	EST_HUMAN	QV4-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4410	17438	30326	5.3	8.0E-03	BF363327.1	EST_HUMAN	CMA-NN0119-300805-223-b05 NN0119 Homo sapiens cDNA
4747	17767	30682	0.65	8.0E-03	P03181	SWISSPROT	HYPOHETICAL BHLFI PROTEIN
4747	17767	30683	0.65	8.0E-03	P03181	SWISSPROT	HYPOHETICAL BHLFI PROTEIN
5001	18697	31698	2.68	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28 (KIFC1, Fas-binding protein, BING1, tapasin, RadGS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21, gene, partial>
6323	25659	32635	1.39	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (27)
6913	16963	33261	4.24	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
7104	20038		1.4	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7415	20382	33733	1.88	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (tag cell), exon 1, 5' end
7760	20743		1.81	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds



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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9235	22201	35631	0.58	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
9261	22227	35657	3.77	8.0E-03	AW809692.1	EST_HUMAN	PRECURSOR (HSPG) (PERLECAN) (PLC)
9270	22236	35665	0.52	8.0E-03	AL139075.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 2/6
9331	22296	35726	0.38	8.0E-03	978656	NT	Mus musculus tition 2 (human) (Fus2), mRNA
10308	22322		5.16	8.0E-03	BE086509.1	EST_HUMAN	QV1-BT0877-Q0400-131-g03 BT0877 Homo sapiens cDNA
11118	24078	37602	1.96	8.0E-03	BE788441.1	EST_HUMAN	601475019F1 NIH_MGC_081 Homo sapiens cDNA clone IMAGE:3878405 5'
11330	24280		2.65	8.0E-03	Z49652.1	NT	S.cerevisiae chromosome X reading frame ORF YJRI52w
11649	24586	38156	2.50	8.0E-03	BF56327.1	EST_HUMAN	OM44-NN0119-300600-228-305 NN0119 Homo sapiens cDNA
11710	24675	38252	1.35	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NC1_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11710	24675	38253	1.55	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NC1_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
12024	24900	38495	3.74	8.0E-03	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
12205	25047		2.04	8.0E-03	M69035.1	NT	Cyclodagrus cuniculus eIF-2a kinase mRNA, complete cds
12249	25077		2.6	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
695	13757	26887	18.14	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
695	13757	26887	18.14	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
978	14029	26983	4.86	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1118	14162	27113	4.38	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFA2F10 5'
1398	14400		1.18	7.0E-03	Q61080	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3/HPH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1398	14430	27399	3.03	7.0E-03	AA688298.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HNF-2)
1502	14535	27509	3.04	7.0E-03	AW303599.1	EST_HUMAN	ab76009.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:283145 3'
1756	14785	27768	1.03	7.0E-03	AW590556.1	EST_HUMAN	xv21602.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2813739 3'
1756	14785	27770	1.03	7.0E-03	AW590556.1	EST_HUMAN	EST336268 MAGE resequences, MAGEA Homo sapiens cDNA
2267	15988	28307	2.08	7.0E-03	P04929	SWISSPROT	EST336268 MAGE resequences, MAGEA Homo sapiens cDNA
3571	16816	29537	0.87	7.0E-03	AI150273.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3778	16820	29728	0.93	7.0E-03	AW444463.1	EST_HUMAN	q734h02.x1 Soares_test6_NHT Homo sapiens cDNA clone IMAGE:1761955 3'
3825	18865	29769	1.45	7.0E-03	AF196344.1	NT	UI-H813-alk-c-10-Q-U1 s1 NC1_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4048	18820	29728	0.83	7.0E-03	AW444463.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4398	17393		0.66	7.0E-03	U96086.1	NT	Dictyostelium discoideum multidrug resistance transporter/Ser protease (tagC) mRNA, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4555	17598			7.0E-03	AW117711.1	EST_HUMAN	x33409.x1 NC1 CGAP_U1 Homo sapiens cDNA clone IMAGE:2609033 3' similar to TR:Q12897 Q12897 ACIDIC 82 KDA PROTEIN. ;
4629	17650		1.47	7.0E-03	AW303898.1	EST_HUMAN	h89405.y1 NC1 CGAP_GU1 Homo sapiens cDNA clone IMAGE:2866536 5'
5024	18038		1.81	7.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5226	18234	31108	1.4	7.0E-03	AV724419.1	EST_HUMAN	AV724419 HTB Homo sapiens cDNA clone HTBCE08 5'
5228	18234	31108	1.4	7.0E-03	AV724419.1	EST_HUMAN	AV724419 HTB Homo sapiens cDNA clone HTBCE08 5'
5918	19004		0.83	7.0E-03	H71108.1	EST_HUMAN	y82901.1.1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:211824 5' similar to
6233	25656		5.11	7.0E-03	AW851058.1	EST_HUMAN	g6x14723 CLUSTERIN PRECURSOR (HUMAN);
6447	19512	32762	1.38	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0288-056400-018-008 CT0288 Homo sapiens cDNA
6687	19744	33019	3.16	7.0E-03	AA327129.1	EST_HUMAN	z63310.r1 Scores_fetal Heart_NBHH18W Homo sapiens cDNA clone IMAGE:342475 5'
6717	19773	33052	0.91	7.0E-03	BE857385.1	EST_HUMAN	7q34b10.x1 NC1 CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13397
7284	20061	33367	1.82	7.0E-03	BE528133.1	EST_HUMAN	Q13397 HYPOTHETICAL PROTEIN 354D8_2, contains TAR1.2 TAR1 TAR1 repetitive element ;
7763	20716	34088	5.31	7.0E-03	Z35638.1	NT	GMP-CT0478-230800-347-511 CT0478 Homo sapiens cDNA
7763	20716	34088	5.31	7.0E-03	Z35638.1	NT	S.cerevisiae chromosome II reading frame ORF_YBL077w
8180	21150	34557	0.45	7.0E-03	AJ226043.1	NT	Homo sapiens 959 kb contig between AML1 and CBRT1 on chromosome 21q22, segment 3/3
8180	21150	34558	0.45	7.0E-03	AJ226043.1	NT	Homo sapiens 959 kb contig between AML1 and CBRT1 on chromosome 21q22, segment 3/3
8448	21417	34830	2.46	7.0E-03	BE175667.1	EST_HUMAN	RC8-HT0582-160300-011-003 HT0582 Homo sapiens cDNA
8961	21627	35394	0.49	7.0E-03	AF281074.1	NT	Homo sapiens neurapillin 2 (NRP2) gene, complete cds, alternatively spliced
9752	22693		0.71	7.0E-03	AF11166.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
9653	22980	36344	0.85	7.0E-03	N52378.1	EST_HUMAN	y446c10.s1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains
10078	23005	36475	2.84	7.0E-03	P48682	SWISSPROT	Alu repetitive element;
10078	23005	36476	2.84	7.0E-03	P48682	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10078	23005	36476	2.84	7.0E-03	P48682	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10698	23590		1.06	7.0E-03	AV687378.1	EST_HUMAN	AV687378 GK Homo sapiens cDNA clone GKCAFC07 5'
10698	23773		0.95	7.0E-03	AV769734.1	EST_HUMAN	wc37c606.x1 NC1 CGAP_P128 Homo sapiens cDNA clone IMAGE:2320430 3'
11175	24132	37662	2.23	7.0E-03	AB308852.1	NT	Bos taurus mRNA for NDPE2, complete cds
11248	24201	37722	1.51	7.0E-03	AJ004662.1	NT	Homo sapiens perlecan MUCSB gene, exon 1-26
11248	24201	37722	1.51	7.0E-03	AJ004662.1	NT	Homo sapiens perlecan MUCSB gene, exon 1-26
12734	25977		1.53	7.0E-03	H94065.1	EST_HUMAN	y715h01.s1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
12741	25991		1.91	7.0E-03	BE263253.1	EST_HUMAN	Alu repetitive element;
12834	25451		1.99	7.0E-03	Y17455.1	NT	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3180478 5'
12834	25451		1.99	7.0E-03	Y17455.1	NT	Homo sapiens LSFR2 gene, penultimate exon

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1245	14282	27244	9.98	8.0E-03	AW511148.1	EST_HUMAN	h22a05.x1 Soares, NFL_T, GBC, S1 Homo sapiens cDNA clone IMAGE:2610224 3' similar to SW:PXR_HUMAN 075468 ORPHAN NUCLEAR RECEPTOR PXR;
1245	14282	27245	9.96	8.0E-03	AW511148.1	EST_HUMAN	h22a05.x1 Soares, NFL_T, GBC, S1 Homo sapiens cDNA clone IMAGE:2610224 3' similar to SW:PXR_HUMAN 075468 ORPHAN NUCLEAR RECEPTOR PXR;
2762	15774	28793	1.32	6.0E-03	AF112374.1	NT	Danio rerio cdkrent receptor gene cluster
2901	15960	28870	4.82	6.0E-03	AA759135.1	EST_HUMAN	ah78a11.x1 Soares, testis, NHT Homo sapiens cDNA clone 132172 3'
2901	15960	28860	4.82	6.0E-03	AA759135.1	EST_HUMAN	ah78a11.x1 Soares, testis, NHT Homo sapiens cDNA clone 132172 3'
3260	16314		2.26	6.0E-03	H75890.1	EST_HUMAN	y77f04.1 Soares fetal liver spleen, INFLS Homo sapiens cDNA clone IMAGE:211351 5'
3393	16442	26368	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasodilator genes, complete cds
3393	16442	26368	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasodilator genes, complete cds
3557	16603		1.28	6.0E-03	W37685.1	EST_HUMAN	zz13a11.l1 Soares, parathyroid tumor, NHHPA Homo sapiens cDNA clone IMAGE:322172 5'
3672	16715	29629	4.48	6.0E-03	BF510986.1	EST_HUMAN	UJ-H-Bk4-gpm-c-06-0-U1et NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3709	16751	29657	1.21	6.0E-03	BE077356.1	EST_HUMAN	RC1-B100605-260400-014-a07 B10605 Homo sapiens cDNA
3760	16831	29737	1.19	6.0E-03	6754029	NT	Mus musculus glucocorticoid-6-phosphate dehydrogenase (G6p), mRNA
3944	16984	29900	0.87	6.0E-03	AW847284.1	EST_HUMAN	RC9-CT0234-240999-021-b10 CT0204 Homo sapiens cDNA
3979	17019		0.9	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH, MGCC, T5 Homo sapiens cDNA clone IMAGE:2859513 5'
4391	17419		1.81	6.0E-03	A016833.1	EST_HUMAN	oa32c11.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4724	17744	30635	5.97	6.0E-03	AA324242.1	EST_HUMAN	EST127116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
6276	25657	32581	0.9	6.0E-03	5827621	NT	Varicella virus, complete genome
6989	20212	33541	0.87	6.0E-03	O14684	SWISSPROT	SYNAPSIN III
7034	18066	31253	0.84	6.0E-03	BE263748.1	EST_HUMAN	601112353F1 NIH, MGCC, T8 Homo sapiens cDNA clone IMAGE:3383172 5'
7461	20427	33783	0.93	6.0E-03	AA269442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7461	20427	33784	0.93	6.0E-03	AA269442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7908	20851	34238	0.83	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
8100	21036	34436	0.82	6.0E-03	P17594	SWISSPROT	RAS-RELATED PROTEIN RAP-2B
8136	21073	34473	0.5	6.0E-03	AJ243211.1	NT	Homo sapiens DMRT1 candidate tumor suppressor gene, exons 1 to 55
8191	21161	34571	6.56	6.0E-03	AJ033890.1	EST_HUMAN	owl3a0.4.x1 Soares, parathyroid tumor, NHHPA Homo sapiens cDNA clone IMAGE:1646870 3' similar to contains MER10.b1 MEK10 repetitive element;
8307	21276	34687	2.54	6.0E-03	AF709337.1	EST_HUMAN	RC9-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
8381	21350		1.51	6.0E-03	BF038198.1	EST_HUMAN	60145495F1 NIH, MGCC, 96 Homo sapiens cDNA clone IMAGE:3688828 5'
9912	22733	35198	8.57	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein

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Table 4  
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10403	23325		2.08	6.0E-03	AI432861.1	EST_HUMAN	U22022.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SWR19A_HUMAN
10523	23449	38943	0.87	6.0E-03	AJ011849.1	NT	P40428 60S RIBOSOMAL PROTEIN L13A ; Bacillus subtilis fmd gene
10659	23581		1.03	6.0E-03	AF084555.1	NT	Homo sapiens oleic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10769	23690	37187	0.68	6.0E-03	X83068.1	NT	M thermophilum complete plasmid pP1 DNA
11096	24066	37580	1.61	6.0E-03	AB92164.1	EST_HUMAN	EST1374237 MAGE resequences, MAGE Homo sapiens cDNA
11162	24120		1.55	6.0E-03	1T545814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
11327	24277		3.99	6.0E-03	U14556.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
11328	24278	37805	2.55	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3539747 5'
12319	25123		2.28	6.0E-03	AF010485.1	NT	Rhodospirillum rubrum strain S91003, partial genome
12422	25812		1.62	6.0E-03	BF571185.1	EST_HUMAN	602151024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292212 5'
12446	25744		5.28	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450298 (section 39 of 148) of the complete genome
12526	25807		2.71	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pg1) gene, complete cds
12576	26285		1.48	6.0E-03	Q82208	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1) PROTEIN
12850	25459		2.18	6.0E-03	BE788019.1	EST_HUMAN	601482821F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3885388 5'
12869	25471		1.53	6.0E-03	AJ245490.1	NT	Brassica napus alg gene for S-luciferase, cultivar T2
13043	25584		1.76	6.0E-03	BF110286.1	EST_HUMAN	7n35b1.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:356564 3'
670	13735	26861	2.34	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORF8, and grpE-like protein, complete cds
670	13736	26862	2.34	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORF8, and grpE-like protein, complete cds
671	13735	26861	3.43	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORF8, and grpE-like protein, complete cds
671	13736	26862	3.43	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORF8, and grpE-like protein, complete cds
1114	14158	27109	1.03	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
1574	14607		1.02	5.0E-03	A1138977.1	EST_HUMAN	q77605.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2890	15686	28703	2.63	5.0E-03	AB333006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2947	16005	28830	3.66	5.0E-03	BE266057.1	EST_HUMAN	601194706F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3153	16210	29125	3.96	5.0E-03	T87623.1	EST_HUMAN	y83105.x1 Soares Infant brain (NIH Homo sapiens cDNA clone IMAGE:22395 3'
3169	16224		3.05	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3181	10236	29153	1.22	5.0E-03	R71794.1	EST_HUMAN	y88q02.s1 Scars breast 2(NHBT) Homo sapiens cDNA clone IMAGE:156688 3'
3291	18344		0.94	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0861 gene
3679	16722	28635	0.97	5.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
3713	16766	29670	4.03	5.0E-03	AF14749.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3771	16813	29722		5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
3965	17035		2	5.0E-03	AA296678.1	EST_HUMAN	U121218 Uterus tumor 1 Homo sapiens cDNA 5' end
4333	17361	30246	0.69	5.0E-03	H78355.1	EST_HUMAN	y17970.0.1 Scars fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:240066 5'
4335	18313	29722	1.02	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4601	17622	30515	1.02	5.0E-03	U46991.1	NT	Human putative chromatin structure regulator (SUT6H) mRNA, complete cds
4638	17659	30546	1.13	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4749	17769	30665	1.34	5.0E-03	A1752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
4970	17985	30875	1.06	5.0E-03	P15265	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
5223	18230	31105	1.69	5.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gpd), mRNA
5653	18981	32172	5.59	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROBABLE UBQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBQUITIN THIOLESTERASE FAF-Y) (UBQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBQUITIN-SPECIFIC PROTEASE 8, Y CHROMOSOME)
6162	19237	32468	2.97	5.0E-03	O00507	SWISSPROT	Chlamydia pneumoniae AR39, section 82 of 84 of the complete genome
6168	19272		0.89	5.0E-03	AE002234.2	NT	B00944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960871 3'
6747	19801		7.44	5.0E-03	BE300091.1	EST_HUMAN	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
7023	18355	31274	7.12	5.0E-03	AB025024.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7240	19975		0.82	5.0E-03	AB038267.1	NT	
7295	20267	33602	0.57	5.0E-03	6753651	NT	Mus musculus dyx11, exon, heavy chain 11 (Dyxl11), mRNA
7727	20683	34047	0.62	5.0E-03	T05124.1	EST_HUMAN	EST103012 Fetal brain, Stragaine (cat#936206) Homo sapiens cDNA clone HFBCR93 similar to EST containing Alu repeat
7856	20801		1.17	5.0E-03	AW854327.1	EST_HUMAN	RC3-C10255-031099-011-107 CT0255 Homo sapiens cDNA
8044	20981	34378	6.8	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8097	21033	34431	0.49	5.0E-03	Q9R001	SWISSPROT	ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS) (AGGREGANASE-2) (ADMP-2) (IMPLANTIN)
8097	21033	34432	0.49	5.0E-03	Q9R001	SWISSPROT	ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS) (AGGREGANASE-2) (ADMP-2) (IMPLANTIN)
8581	21549	34967	2.12	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8659	21925		5.83	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9159	22126	35554	1.08	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA. (19.1 - 19.4 min)
9292	22256	35698	0.81	5.0E-03	M25090.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
10199	23124	36811	0.97	5.0E-03	L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
10330	23254	36732	0.68	5.0E-03	AW821838.1	EST_HUMAN	RCO-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10318	23440	36938	0.44	5.0E-03	AA533143.1	EST_HUMAN	nm4810.61 NCI CGAP P19 Homo sapiens cDNA clone IMAGE:965687
10896	23618	37112	0.47	5.0E-03	762257	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10844	23764		0.51	5.0E-03	AA653261.1	EST_HUMAN	ig49c10.61 Gesler Wilms tumor Homo sapiens cDNA clone IMAGE:1126280 3'
11075	24037		4.17	5.0E-03	T19966.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
11287	24237	37764	2.15	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares, NIH/CaC, cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1 L2 L1 repetitive element :
11287	24237	37765	2.15	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares, NIH/CaC, cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1 L2 L1 repetitive element :
11381	24328	37857	1.55	5.0E-03	T49153.1	EST_HUMAN	y609e04.r1 Stratagene placenta (#637225) Homo sapiens cDNA clone IMAGE:70686 5'
11659	24595		3.62	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.r1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:2291622 5'
12463	25038		5.42	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12593	25298		3.7	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12688	25355		3.19	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exon 1-54, complete cds
12716	25372		1.89	5.0E-03	AA456597.1	EST_HUMAN	zk75603.s1 Soares, over tumor Nihhot Homo sapiens cDNA clone IMAGE:809846 3' similar to SW DXA2 MOUSE P14693 PROBABLE DIPHENOL OXIDASE A2 COMPONENT :
12743	25752		5.67	5.0E-03	BF57232.1	EST_HUMAN	60207774F1 NIH MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
12922	25498	31702	3.21	5.0E-03	AW449109.1	EST_HUMAN	UHLB193-akf4-08-CJ1.1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2794215 3'
235	13335	26259	2.6	4.0E-03	AW500196.1	EST_HUMAN	UHLB193-akf4-08-CJ1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076931 5'
321	13413	26337	2.12	4.0E-03	R46482.1	EST_HUMAN	UHLB193-akf4-08-CJ1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076931 5'
443	13516	26449	1.15	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
605	13672	26566	4.63	4.0E-03	AA598339.1	EST_HUMAN	on75012.s1 Soares, NFL, T, GBC S1 Homo sapiens cDNA clone IMAGE:1562566 3'
678	13933	26893	1.9	4.0E-03	R46482.1	EST_HUMAN	y651e04.s1 Soares, infant brain 1N1B Homo sapiens cDNA clone IMAGE:356988 3'
912	13957		3.64	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-R1 BT0333 Homo sapiens cDNA
1153	14165	27147	27.01	4.0E-03	AA099777.1	EST_HUMAN	R81e08.r1 Stratagene cdont (#637204) Homo sapiens cDNA clone IMAGE:510988 5'
1173	14214	27169	1.92	4.0E-03	AW764740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1306	14342	27306	1.5	4.0E-03	AA284374.1	EST_HUMAN	z559a01.r1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:701736 5'
1890	14622		1.64	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone IMAGE:1562566 3'
1759	14787	27772	2.38	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds
2034	15053	28070	11.42	4.0E-03	AA099777.1	EST_HUMAN	z81e08.r1 Stratagene cdont (#637204) Homo sapiens cDNA clone IMAGE:510988 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2259	15273		1.66	4.0E-03	BE410586.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2266	15299	28323	1.53	4.0E-03	AW794740.1	EST_HUMAN	RC8-UN0014-170400-023-G01 UN0014 Homo sapiens cDNA
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc2/Cdkmodulin-dependent protein kinase 1 (CAK/K1), creatine transporter (CRTTR), CDM protein (CDM), adenoleukodystrophy protein >
2579	15590	26598	1.75	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc2/Cdkmodulin-dependent protein kinase 1 (CAK/K1), creatine transporter (CRTTR), CDM protein (CDM), adenoleukodystrophy protein >
2579	15590	28598	1.75	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc2/Cdkmodulin-dependent protein kinase 1 (CAK/K1), creatine transporter (CRTTR), CDM protein (CDM), adenoleukodystrophy protein >
2701	15697	28712	3.92	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing G14ORF4 gene
2701	15697	28713	3.92	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing G14ORF4 gene
2707	15702	28716	1.68	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS210284
3239	16204	29217	1.04	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151298-003-H08 HT0340 Homo sapiens cDNA
3239	16294	29218	1.04	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151298-003-H08 HT0340 Homo sapiens cDNA
3541	16587	29510	0.8	4.0E-03	AW188426.1	EST_HUMAN	X9804.x1 NCI CGAP Cor18 Homo sapiens cDNA clone IMAGE:2665278 3'
3541	16587	29511	0.8	4.0E-03	AW188426.1	EST_HUMAN	X9804.x1 NCI CGAP Cor18 Homo sapiens cDNA clone IMAGE:2665278 3'
3639	16682	29697	0.84	4.0E-03	Q13606	SWISSPROT	OLFACATORY RECEPTOR 811 (OLFACATORY RECEPTOR-LIKE PROTEIN OLF1)
4020	17058		2.14	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4643	17864	30553	1.1	4.0E-03	AJ732754.1	EST_HUMAN	ab1808.x6 Stratagene lung (H937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains ALU repetitive element.
4805	17822	30717	3.73	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS210284
5173	18182	31050	0.98	4.0E-03	AW103719.1	EST_HUMAN	X683403.x1 NCI CGAP Bm35 Homo sapiens cDNA clone IMAGE:2814469 3' similar to contains L1.11 L1 L1 repetitive element.
5220	18228	31102	0.63	4.0E-03	AA695995.1	EST_HUMAN	Z169401.x1 Sources fetal liver spleen 1NFSL S1 Homo sapiens cDNA clone IMAGE:436009 3'
5272	18278	31142	0.93	4.0E-03	J02187.1	NT	Foot and mouth disease virus serotype A-12 198b capsid protein VP3
5348	18453	31324	1.96	4.0E-03	AF005889.1	NT	Drosophila melanogaster arn-207 (arn-207) mRNA, complete cds
5473	18493	31462	23.1	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5991	18979	32171	2.72	4.0E-03	P04196	SWISSPROT	(HPRG)
5995	18983	32173	1.63	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOZOTIC ANTIGEN PRECURSOR
5983	19068	32266	0.97	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7611014.1_1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp7611014 5'
6203	19277		3.98	4.0E-03	J22180.1	NT	Rattus norvegicus opsin gene, complete cds
6301	19430	32673	1	4.0E-03	AW590572.1	EST_HUMAN	hg68007.x1 NCI CGAP G08 Homo sapiens cDNA clone IMAGE:2048652 3'
6442	19507	32757	1.78	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3481954 5'
6827	19881	33172	0.87	4.0E-03	AA813222.1	EST_HUMAN	aj3211.x1 Sources testis_NHT Homo sapiens cDNA clone 1392045 3'
6842	20168	33489	1.5	4.0E-03	U75408.1	NT	Lycopodium obscurum knotted 3 protein (TK03) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7273	20008	33308	1.22	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C0078
7273	20008	33309	1.22	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C0078
7404	20372	33723	4.12	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7665	20824	33968	0.99	4.0E-03	A0681483.1	EST_HUMAN	h37g12x1 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7667	20826	33950	0.72	4.0E-03	BE570170.1	EST_HUMAN	7631b02.x1 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7767	20720		0.68	4.0E-03	X92106.1	NT	H. sapiens hspX gene
8274	21243	34655	0.48	4.0E-03	Q8T792	SWISSPROT	ADAM-15 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
8393	21352	34761	5.06	4.0E-03	AFT11944.1	NT	Dilatystallium discordeum AX4 development protein DG1122 (DG1122) gene, partial cds
8545	21513	34930	1.92	4.0E-03	7652067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
9064	22030	35453	7.41	4.0E-03	AI553983.1	EST_HUMAN	h49b11.x1 Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:2080013 3' similar to contains Alu repetitive element
9241	22207		4.72	4.0E-03	AL163269.2	NT	Homo sapiens chromosome 21 segment HS21C009
9250	22216	35646	3.68	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C0078
10287	23212	36695	0.57	4.0E-03	H00664.1	EST_HUMAN	h42g12.1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190150 5'
10742	23664	37159	0.79	4.0E-03	AL161553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11176	24133	37663	1.65	4.0E-03	AW613635.1	EST_HUMAN	h47h04.x1 NC1 CGAP LH1 Homo sapiens cDNA clone IMAGE:2707159 3'
11464	24407	37954	4.53	4.0E-03	AL163269.2	NT	Homo sapiens chromosome 21 segment HS21C008
12431	26966		1.52	4.0E-03	BE815173.1	EST_HUMAN	PMH-BN0138-160500-002-b08 BN0138 Homo sapiens cDNA
12454	25213		3.2	4.0E-03	BE288590.1	EST_HUMAN	h01118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12533	25259		2.13	4.0E-03	AW504273.1	EST_HUMAN	UHF-BN0-slp-9-04-GJ1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080822 5'
12755	25400		7.22	4.0E-03	BF224125.1	EST_HUMAN	h74cd09.x1 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element
12801	29886		3.31	4.0E-03	AW614596.1	EST_HUMAN	h02d07.x1 NC1 CGAP_KH11 Homo sapiens cDNA clone IMAGE:28553932 3' similar to contains element LTR9 repetitive element
12814	25437		2.73	4.0E-03	AW619141.1	EST_HUMAN	RC3-ST0281-240-400-015-03 ST0281 Homo sapiens cDNA
13053	25619	31675	6.48	4.0E-03	11436955	NT	Homo sapiens G12-associated binder 2 (KIA0571), mRNA
371	13457	26387	1.69	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
880	13935	26394	3.09	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1669	14701	27676	5.52	3.0E-03	AA468110.1	EST_HUMAN	h073cd05.x1 NC1 CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element
2268	15281		1.58	3.0E-03	AF050665.1	NT	Homo sapiens MHC class 1 region
2302	15314		8.08	3.0E-03	Z32521.1	NT	S. cereale (cv. Hilo) mRNA for bisphosphate isomerase
2303	15315	28334	1.3	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds



Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2303	15315	28335	1.3	3.0E-03	U4658.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3005	19084		0.8	3.0E-03	Y09005.1	NT	Arabidopsis thaliana rpoM1 gene
3090	16156	29069	4.09	3.0E-03	BE379286.1	EST_HUMAN	G01237822-1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3168	16221	29138	2.54	3.0E-03	AW802687.1	EST_HUMAN	IL2-JM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3428	16478	28395	1.62	3.0E-03	U34908.1	NT	Mus musculus alpha-(XVIII) collagen (COL18A1) gene, exon 1 and 2
3439	16486		6.72	3.0E-03	Y12500.1	NT	Celegans smad6 gene
4002	17041	29949	7.18	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDS95G01 5'
4002	17041	29950	7.18	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDS95G01 5'
4087	17103	29995	1.47	3.0E-03	AT92278.1	EST_HUMAN	ad0409.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4177	17208					NT	S cereale (cv. Halo) mRNA for triosephosphate isomerase
4424	17451	30342	3.8	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4546	17580	30438	5.58	3.0E-03	AI536141.1	EST_HUMAN	xb8.P10.H3 conorm Homo sapiens cDNA 3'
4874	17888	30776	1.74	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.v5 Srsfapene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4990	17907	30798	5.49	3.0E-03	BE787945.1	EST_HUMAN	G01482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5338	18443	31196	3.42	3.0E-03	8922469	NT	Homo sapiens hypothetical protein FLJ10639 (FLJ10639), mRNA
5535	18731	31893	1.22	3.0E-03	AJ246981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5708	18803	31890	0.95	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6705	19761	33040	10.04	3.0E-03	AA466701.1	EST_HUMAN	Agg10101 Scores: NHHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7224	20246	33580	0.65	3.0E-03	D37877.1	NT	Fugu rubripes mRNA for sodium channel alpha subunit, partial cds
7412	20379	33730	1.37	3.0E-03	AJ011416.1	NT	Kluweromyces mandarinus pop3 gene for purine-cytosine permease
7765	20718	34091	3.16	3.0E-03	AB021736.1	NT	Oryza sativa gene for LZIP protein, complete cds
8145	21082	34431	0.49	3.0E-03	P28659	SWISSPROT	DNA REPAIR HELICASE RAD15 (RHP3)
8270	21239	34650	0.91	3.0E-03	BF333058.1	EST_HUMAN	RC0-BT0812-250600-032-407 BT0812 Homo sapiens cDNA
8270	21248	34651	0.91	3.0E-03	BF333058.1	EST_HUMAN	RC0-BT0812-250600-032-407 BT0812 Homo sapiens cDNA
8498	21464	34880	1.31	3.0E-03	N92560.1	EST_HUMAN	zb27604.s1 Scores: parathyroid_tumor_NHHpA Homo sapiens cDNA clone IMAGE:304783 3'
8553	21626		0.77	3.0E-03	M63498.1	NT	S cerevisiae UGA35 gene, complete cds
8804	21771	35197	1.16	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2A1)
8827	21784	35217	1.34	3.0E-03	AI163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8833	21899		1.25	3.0E-03	Q9QMB1	SWISSPROT	NONSTRUCTURAL PROTEIN V
9343	22308					EST_HUMAN	h180F0.X1 NC1 CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1.1 L1 repetitive element
9400	22365	35797	4.01	3.0E-03	AL161569.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9424	22388	35927	4.74	3.0E-03	A016731.1	EST_HUMAN	ov33d12.x1 NCL CGAP_K143 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb-X67138_ma1
9434	22398	35836	0.83	3.0E-03	BF339078.1	EST_HUMAN	H1STONE H2B.2 (HUMAN);
9764	22705		0.95	3.0E-03	D90301.1	NT	60203660F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183593 5'
9802	22128	34529	0.61	3.0E-03	BE154870.1	EST_HUMAN	Synchocystis sp. PC36803 complete genome, 3127, 271600-402289
9894	22921		0.62	3.0E-03	P03355	SWISSPROT	PM3-H1T0344-071299-003-407 H1T0344 Homo sapiens cDNA
10085	22892		5.33	3.0E-03	P03672	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H] CIRCUMSPOROZOTE PROTEIN PRECURSOR (CS)
10255	23180	36667	1.56	3.0E-03	P11389	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
10355	23279	36755	1.15	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10499	23421	36920	4.39	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS2TCT03
11194	24149		1.62	3.0E-03	5903028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11708	24673	38250	1.47	3.0E-03	AF008222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
11775	23930	37451	1.86	3.0E-03	AF286285.1	NT	Homo sapiens galgin-like protein (GLP) gene, complete cds
11810	24695	38278	2.27	3.0E-03	AF094481.1	NT	Homo sapiens thymidine repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11810	24695	38278	2.27	3.0E-03	AF094481.1	NT	Homo sapiens thymidine repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11881	24763	38348	1.47	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
12199	25795		4.08	3.0E-03	A1525058.1	EST_HUMAN	protonin-5.E07.r1 tumor Homo sapiens cDNA 5'
12232	25004	38162	1.83	3.0E-03	AA593154.1	EST_HUMAN	ot710.1 at Soares_Jdel Telus_Nb2HF8_Sw Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER28 repetitive element;
12292	25895		2.42	3.0E-03	AB009568.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
12478	25228	31704	2.01	3.0E-03	AJ266282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
516	13587	26506	0.92	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
518	13587	26507	0.92	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
786	15851		12.64	2.0E-03	T70874.1	EST_HUMAN	yt15h03.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:108341 5'
1365	14399	27370	1.19	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1368	14402	27372	1.34	2.0E-03	AA561505.1	EST_HUMAN	nu5670.1 s1 NCL CGAP_Av1 Homo sapiens cDNA clone IMAGE:1217593
1376	14410	27380	12.34	2.0E-03	AJ284448.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1486	14519	27492	1.63	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SPA-1) (CD161 ANTIGEN)
1519	14551	27522	3.03	2.0E-03		NT	Homo sapiens procollagen-lysin, 2-oxoglutarate 6-oxoglutarate (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (FLOD) mRNA

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1519	14551	27523	3.03	2.0E-03	4557836	NT	Homo sapiens procollagen-lysin, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (P10D) mRNA
1595	14927		8.7	2.0E-03	P28400	SWISSPROT	COLLAGEN ALPHA 9(V) CHAIN PRECURSOR
1786	14815	27800	1.26	2.0E-03	AA450138.1	EST_HUMAN	X42420.11 Soares, total, fetus, NB2HFB, 9w Homo sapiens cDNA clone IMAGE:786114 5'
2011	15032	28042	1.32	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2261	15275	28269	1.02	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2364	15595		4.02	2.0E-03	AW13782.1	EST_HUMAN	U1-HB11-adj-g-10-Q-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3427	16475	28394	4.82	2.0E-03	AA450138.1	EST_HUMAN	X42420.11 Soares, total, fetus, NB2HFB, 9w Homo sapiens cDNA clone IMAGE:786114 5'
3434	16481	29400	0.8	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3680	16723	29636	6.1	2.0E-03	X57344.1	NT	H sapiens DNA, DMB1, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
3973	17013	29927	0.85	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4140	17171	30059	2.1	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP32; COAT PROTEIN GP38]
4203	17234	30122	1.26	2.0E-03	AA179693.1	EST_HUMAN	xp13101.11 Stragena fetal retina 837202 Homo sapiens cDNA clone IMAGE:509361 5'
4248	17277		9.31	2.0E-03	U08491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4458	17484		1.01	2.0E-03	AW287390.1	EST_HUMAN	U1-HBW0-air-g-03-Q-U1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:2730413 3'
4462	17486	30375	1.11	2.0E-03	AI064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4577	17599	30493	1.99	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4577	17599	30494	1.99	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4735	17765	30649	1.09	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4740	17760		1.84	2.0E-03	R87773.1	EST_HUMAN	y045602.s1 Soares adult brain NB2HAB557 Homo sapiens cDNA clone IMAGE:180890 3'
5054	18066	30945	0.75	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5163	18172	31051	1.02	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
5281	18287	31149	2.26	2.0E-03	D05606.1	NT	Homo sapiens gene for cholecystikinin type-A receptor, complete cds
5594	18661	31607	1.33	2.0E-03	BF241410.1	EST_HUMAN	601878355F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5709	25643	31981	2.18	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0963 protein, partial cds
5795	18887	32098	0.61	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-022 UM0025 Homo sapiens cDNA
5795	18887	32099	0.61	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-022 UM0025 Homo sapiens cDNA
5797	18889	32071	1.73	2.0E-03	U063711.1	NT	Xenopus laevis xellin mRNA, complete cds
6231	18905	32536	3.76	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6231	18905	32537	3.79	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6480	18945	32793	15.16	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6480	19545	32794	15.16	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6482	19547	32796	7.38	2.0E-03	BF308187.1	EST_HUMAN	6011897434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6521	19584	32842	2.26	2.0E-03	Q9UKP4	SWISSPROT	ADAMTS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6522	19585	32843	0.77	2.0E-03	AV706075.1	EST_HUMAN	AV706075 ADG Homo sapiens cDNA clone ADOAEF09 5'
6554	19614	32878	1.36	2.0E-03	X94451.1	NT	L esculentum mRNA for lpsyl-rRNA synthetase (LYRS)
6756	19810						wu36109.x1 Soares_Dickgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW-RL26_HUMAN P47914 60S RIBOSOMAL PROTEIN L26 contains element MSRT repetitive element ;
6794	19848	33133	0.71	2.0E-03	AA677831.1	EST_HUMAN	TZ13at1.x1 Soares_Fetal Liver spleen_INFUS_S1 Homo sapiens cDNA clone IMAGE:430852 3'
7151	18383	31271	1.08	2.0E-03	AB038502.1	NT	Cacanthobittis elegans mRNA for galactin LEC-11, complete cds
7287	20084	33371	2.86	2.0E-03	BE067866.1	EST_HUMAN	CMA-BT0306-061299-054-401 BT0306 Homo sapiens cDNA
7351	20321	33508	0.64	2.0E-03	A1268883.1	EST_HUMAN	q98d11.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:183885 3'
7511	20476	33837	0.77	2.0E-03	T86568.1	EST_HUMAN	y477g10.t1 Soares_fetal liver spleen_INFUS_Homo sapiens cDNA clone IMAGE:114308 5'
7877	20821	34198	1.55	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8386	21355	34763	1.95	2.0E-03	AW592004.1	EST_HUMAN	h37508.x1 Soares_INFUS_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR-Q60978 Q60978 JERKY. ;
8560	21528	34947	6.01	2.0E-03	N20287.1	EST_HUMAN	y429d06.s1 Soares_melanocyte_2NHLM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8560	21528	34948	6.01	2.0E-03	N20287.1	EST_HUMAN	y429d06.s1 Soares_melanocyte_2NHLM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8607	21575	34960	0.57	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN CG9.05 IN CHROMOSOME I
8629	21597	35018	1.23	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8684	21652	35074	0.77	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPE-1), mRNA
8684	21652	35075	0.77	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPE-1), mRNA
8709	21677	35102	0.81	2.0E-03	AU136879.1	EST_HUMAN	AU136879 PLACET Homo sapiens cDNA clone PLACE1004838 5'
8762	21729		0.67	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
9550	18887	32098	0.66	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-002 UM0025 Homo sapiens cDNA
9550	18887	32098	0.66	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-002 UM0025 Homo sapiens cDNA
9695	22557	36007	0.66	2.0E-03	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9884	22837	36291	0.97	2.0E-03	H50832.1	EST_HUMAN	y86d09.s1 Soares_fetal liver spleen_INFUS_Homo sapiens cDNA clone IMAGE:194298 3'
9884	22837	36292	0.97	2.0E-03	H50832.1	EST_HUMAN	y86d09.s1 Soares_fetal liver spleen_INFUS_Homo sapiens cDNA clone IMAGE:194298 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9916	22737	36190	3.31	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEF) (JI) (MOTENDINUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
10026	22853	38421	1.02	2.0E-03	P48962	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10026	22953	38422	1.02	2.0E-03	P48962	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10051	23008	38479	0.65	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL-10) gene, complete cds
10051	23008	38480	0.65	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL-10) gene, complete cds
10075	23200	36684	0.94	2.0E-03	AF084268.1	EST_HUMAN	QV5-0/T0084-050/400-144-b01 OT0084 Homo sapiens cDNA
10275	23200	36684	0.94	2.0E-03	AF084268.1	EST_HUMAN	QV5-0/T0084-050/400-144-b01 OT0084 Homo sapiens cDNA
10402	23724	37200	0.45	2.0E-03	AA251376.1	EST_HUMAN	zsf0a05 nt NCL CGAP GC91 Homo sapiens cDNA clone IMAGE:684754 3'
10751	23702	37200	0.45	2.0E-03	BF367366.1	EST_HUMAN	MR2-GN0030-140900-001-a05 GN0030 Homo sapiens cDNA
10969	23686	37401	0.43	2.0E-03	AW351176.1	EST_HUMAN	RC1-CT0251-141059-012-b01 CT0251 Homo sapiens cDNA
10969	23686	37402	0.43	2.0E-03	AW351176.1	EST_HUMAN	RC1-CT0251-141059-012-b01 CT0251 Homo sapiens cDNA
11356	24306	37402	2.4	2.0E-03	M85524.1	NT	Human dystrophin gene
11877	20521	34198	2.2	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11870	24752	38342	1.87	2.0E-03	BF330909.1	EST_HUMAN	RC2-BT0333-310800-116-g04 BT0333 Homo sapiens cDNA
11876	24758	38342	10.47	2.0E-03	Z11740.1	NT	H sapiens variable number tandem repeat (VNTR) locus DNA
12180	25028	38623	2.99	2.0E-03	AI625745.1	EST_HUMAN	V65h03.x1 NCL CGAP Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
12197	25042	38623	2.41	2.0E-03	AF157516.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ; Homo sapiens SEL1L (SEL1L) gene, partial cds
12220	25057	38627	1.75	2.0E-03	AI084325.1	EST_HUMAN	o4y3g06.s1 Soares_papillary_tumor_NBIHPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to TR:P97535 P97535 PS-PLA1 PRECURSOR ;
12241	18349		11.57	2.0E-03	AJ245167.1	NT	Canine diomedeanus cvr19 gene for immunoglobulin heavy chain variable region
12459	25032		2.03	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKG Homo sapiens cDNA clone GKGX005 5'
12550	25273	31777	1.93	2.0E-03	Y00508.1	NT	H sapiens MT gene for muscarinic acetylcholine receptor
12663	25341		1.33	2.0E-03	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12710	25785		1.55	2.0E-03	AI375037.1	EST_HUMAN	tf6802.x1 Soares_tzai_fetus_Nb2-IP8_gw Homo sapiens cDNA clone IMAGE:2049051 3' similar to contains Alu repetitive element;
12825	25445		1.6	2.0E-03	AF129756.1	NT	Homo sapiens MSH45 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT14, G4, Apo M, BAT3, BAT2, AIP-1, 1C7, L1-1, L1B, TNF, and LTA genes, complete cds
13002	25745		1.95	2.0E-03	AF097966.1	EST_HUMAN	AV697966 GKG Homo sapiens cDNA clone GKGX005 5'
13095	25621		1.44	2.0E-03	P04797	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH)
439	13513	28444	1.72	1.0E-03	H06471.1	EST_HUMAN	V68608.1 Soares_pneal_gland_NBIHPG Homo sapiens cDNA clone IMAGE:232334 5'

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Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
830	13887	28842	2.09	1.0E-03	AI720263.1	EST_HUMAN	as701008.x1 Barlaid colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825
830	13887	28843	2.09	1.0E-03	AI720263.1	EST_HUMAN	Q13825 AL-BINDING PROTEINEMOYL-COA HYDRATASE ;
1097	14141	27091	3.37	1.0E-03	AI885788.1	EST_HUMAN	as705088.x1 Barlaid colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825
1117	14161	27112	1.69	1.0E-03	AI954572.1	EST_HUMAN	Q13825 AL-BINDING PROTEINEMOYL-COA HYDRATASE ;
1170	14211	27185	1.5	1.0E-03	AI820516.1	EST_HUMAN	wk86063.x1 NCI CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2422288 3'
2042	15051	28032	3.08	1.0E-03	AJ7808	SWISSPROT	wk86101.x1 NCI CGAP_Mat16 Homo sapiens cDNA clone IMAGE:2851242 3'
2163	15179	28186	9.01	1.0E-03	AJ131016.1	NT	repetitive element,
2893	16051	28972	1.42	1.0E-03	AB033117.1	NT	Homo sapiens SCL gene locus
3205	16260	29179	2.08	1.0E-03	P188915	SWISSPROT	Homo sapiens mRNA for KIAA1281 protein, partial cds
3205	16260	29180	2.08	1.0E-03	P188915	SWISSPROT	Homo sapiens mRNA for KIAA1281 protein, partial cds
3313	16366	29296	1.23	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3553	16596	29524	0.92	1.0E-03	U69081.1	NT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3553	16596	29525	0.92	1.0E-03	U69081.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3578	16721		1.49	1.0E-03	AB044400.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3946	16986	29901	0.64	1.0E-03	AW170552.1	EST_HUMAN	Human MUC2 gene, promoter region
3954	16994	29910	1.11	1.0E-03	Z49649.1	NT	Human sapiens SVMT gene for synaptic vesicle monomeric transporter, exon 14, 15
4464	17490	30377	2.27	1.0E-03	BE938162.1	EST_HUMAN	contains TAR1.L1 TAR1 repetitive element ;
4502	17527	30412	4.39	1.0E-03	BE246536.1	EST_HUMAN	S cerevisiae chromosome X, reading frame ORF Y.R148w
4692	17713	30608	0.79	1.0E-03	U29449.1	NT	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4691	17878	30795	2.07	1.0E-03	AI073465.1	EST_HUMAN	TCSAP1D4609 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCSA Homo sapiens cDNA
4691	17878	30796	2.07	1.0E-03	AI073465.1	EST_HUMAN	sapiens cDNA clone TC8AP-4909
4882	17879		4.33	1.0E-03	BE154067.1	EST_HUMAN	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
5113	18123	30998	9.53	1.0E-03	O46409	SWISSPROT	ov45604.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640282 3'
5202	18211	31350	1.03	1.0E-03	AA685870.1	EST_HUMAN	ov45604.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640282 3'
5391	18465	31360	1.74	1.0E-03	AA290551.1	EST_HUMAN	PM0-HT0339-200400-Q10-D02 HT0339 Homo sapiens cDNA
5476	18577	31486	2.98	1.0E-03	AJ006346.1	NT	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
5531	18626	31565	1.77	1.0E-03	K03332.1	NT	AV6885970 GKC Homo sapiens cDNA clone GKCIDME115'
							z544601.c1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700346 5'
							Homo sapiens KVLQ1 gene
							Epsilon-Barr virus (AG878 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5531	18629	31566	1.77	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG878 isolate), U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5552	18748	31916	0.93	1.0E-03	BE796491.1	EST_HUMAN	60186941F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3843954 5'
5658	18754	31921	1.78	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN)
5716	18810	31988	0.7	1.0E-03	N41974.1	EST_HUMAN	y0706.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270387 5' similar to contains element MER0 repetitive element;
5716	18810	31989	0.7	1.0E-03	N41974.1	EST_HUMAN	y0706.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270387 5' similar to contains element MER0 repetitive element;
5995	19079	32276	0.56	1.0E-03	AA773352.1	EST_HUMAN	ab55912.41 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:845734 3'
6018	19101		0.52	1.0E-03	BF541839.1	EST_HUMAN	602068042F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068907 5'
6138	19213		2.97	1.0E-03	X07698.1	NT	Mouse nucleolin gene
6177	19252	32486	1.06	1.0E-03	BE683939.2	EST_HUMAN	601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
6316	19387		8.39	1.0E-03	11526178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
8469	19533	32781	1.05	1.0E-03	T87761.1	EST_HUMAN	y493a11.1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:115772 5'
8549	19610		1.69	1.0E-03	AY802585.1	EST_HUMAN	OV2-NN1024-265400-171-g05 NN1024 Homo sapiens cDNA
8919	19970	33286	1.18	1.0E-03	L77570.1	NT	Homo sapiens D1George syndrome critical region, centromeric and
7359	20326	33678	2.43	1.0E-03	D16826.1	NT	Human gene for fourth semaphorin receptor subtype
7729	20685		2.36	1.0E-03	AJ22604.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
7901	20844	34228	1.71	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc2/Cdkmodulin-dependent protein kinase 1 (CANK1), creatine transporter (CRTFR), CDM protein (CDM), adrenoleukodystrophy protein >
7975	20914	34305	3.18	1.0E-03	M63378.1	NT	Human TRPM2 protein gene, exons 1, 2 and 3
8033	20970	34394	0.87	1.0E-03	BE88044.1	EST_HUMAN	601491081F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3893276 5'
8221	21190	34599	0.55	1.0E-03	AF274581.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
8282	21251	34653	5.32	1.0E-03	AJ251973.1	NT	Homo sapiens partial atoxin-1 gene
8483	21451	34859	1.01	1.0E-03	AA122270.1	EST_HUMAN	2837608.81 Soares_pregnant_uterus_NH-PU Homo sapiens cDNA clone IMAGE:490788 3' similar to contains L1, L1 repetitive element;
8586	21554	34970	2.42	1.0E-03	AF153960.1	NT	Homo sapiens excitase-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8773	21740	35161	0.7	1.0E-03	U26397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8941	21907	35331	0.53	1.0E-03	AA001613.1	EST_HUMAN	2832406.s1 Soares_fetal_liver_spleen_1N1FLS S1 Homo sapiens cDNA clone IMAGE:427810 3'
8941	21907	35332	0.53	1.0E-03	AA001613.1	EST_HUMAN	2832406.s1 Soares_fetal_liver_spleen_1N1FLS S1 Homo sapiens cDNA clone IMAGE:427810 3'
8985	22281		1.37	1.0E-03	Y11204.1	NT	V center gene encoding volvoxin
9321	22286	35716	0.6	1.0E-03	AW840353.1	EST_HUMAN	CMS-LT0079-170200-092-407 LT0079 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9435	22398		0.65	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L16c (RPL16c), Caz-1/Camodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDN protein (CDN), adrenoneurotrophin protein >
9474	22436	35877	3.71	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9474	22438	35878	3.71	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9655	22882		0.45	1.0E-03	A1247482.1	EST_HUMAN	gb56d01.x1 Soares, fetal liver, spleen, 1NfLS, S1 Homo sapiens cDNA clone IMAGE:1948673 3' similar to gbM87388 TATA-BINDING PROTEIN-ASSOCIATED PHOSPHOPROTEIN (HUMAN);
9686	22893	36354	1.77	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (ega) gene, complete cds
8690	22893	36355	1.77	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (ega) gene, complete cds
10179	23104	36585	0.6	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2)(DECORIN) (PG40) (DERMATAN SULFATE
10524	23446	36944	1.55	1.0E-03	AF030329.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10528	23451		0.79	1.0E-03	AF067485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10679	23601	37098	1.12	1.0E-03	A1024350.1	EST_HUMAN	ov75f08.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1
11025	23690	37516	1.65	1.0E-03	AV362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
11025	23690	37517	1.65	1.0E-03	AV362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
11102	24062	37585	2.91	1.0E-03	BE170959.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
11172	24126		2.21	1.0E-03	A1563847.1	EST_HUMAN	tr32a12.x1 NCJ_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26195 Q26195
11491	24434		2.59	1.0E-03	AV755948.1	EST_HUMAN	PVA1 GENE ;
11682	24598	38171	6.18	1.0E-03	AA122270.1	EST_HUMAN	2697c09.x1 Soares, pregnant uterus, Nh-FPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.1t L1 repetitive element ;
12176	25024	38621	6.74	1.0E-03	BE694468.1	EST_HUMAN	501433087F1 NIH_MGC_721 Homo sapiens cDNA clone IMAGE:3818524 5'
12653	25915		1.53	1.0E-03	A1847355.1	EST_HUMAN	tc05h11.x1 NCJ_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element
12753	26806	31311	7.37	1.0E-03	BE780372.1	EST_HUMAN	801468876F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3972035 5'
5765	19857		1.76	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6398	19486		0.81	9.0E-04	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6633	19691	32870	1.08	9.0E-04	P03281	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VARI
10001	22928		1.39	8.0E-04	AB037203.1	NT	Glycerol kinase GpbaS1 mRNA for beta-amylin synthase, complete cds
1484	14517		1.04	8.0E-04	X98465.1	NT	X laevis mRNA for C4SR protein
3539	16979	28804	0.84	8.0E-04	R07008.1	EST_HUMAN	yf21h10.t1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:126891 5'
4209	17258		4.49	8.0E-04	P06547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG



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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4798	17815	30709	2.7	8.0E-04	U29185.1	NT	Homo sapiens priin protein (PRP) gene, complete cds
11480	24423		2.01	8.0E-04	AA77084.1	EST_HUMAN	Z124C10.s1 Soares, fetal heart, NBHH18W Homo sapiens cDNA clone IMAGE:377674 3'
11827	24565		2.02	8.0E-04	AI571096.1	EST_HUMAN	185a03.x1 NCI CGAP_U2 Homo sapiens cDNA clone IMAGE:2176310 3'
1844	14870	27688	1.17	7.0E-04	L41825.1	NT	Homo sapiens CYFIP7 gene, 5' end
2408	15415	28439	1.01	7.0E-04	U29185.1	NT	Homo sapiens priin protein (PRP) gene, complete cds
2728	15720	28737	1.22	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3293	16346	29226	1.13	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
6215	19289	32522	1.02	7.0E-04	AA516212.1	EST_HUMAN	ng5g12.s1 NCI CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.b3 L1 L1 repetitive element1;
6862	19719		2.3	7.0E-04	AI768331.1	EST_HUMAN	wg3606.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
7438	20405		0.78	7.0E-04	AK024445.1	NT	Homo sapiens mRNA for FLJ00335 protein, partial cds
10163	23088	36565	0.48	7.0E-04	P13497	SWISSPROT	BOE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10163	23088	36566	0.48	7.0E-04	P13497	SWISSPROT	BOE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11892	24773		1.98	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FIP3 (FIP3) genes, complete cds
11920	24801	38392	2.41	7.0E-04	Z40561.1	EST_HUMAN	HSC2BA072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12821	25497		4.1	7.0E-04	R17336.1	EST_HUMAN	ygl3c06.r1 Soares infant brain T1B Homo sapiens cDNA clone IMAGE:32268 5'
12852	25627		3.97	7.0E-04	6005955	NT	Homo sapiens Retha-derived POU-domain factor-1 (RPF-1), mRNA
2705	15701		1.03	6.0E-04	BF341380.1	EST_HUMAN	602013339.F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149297 5'
3984	17024	29935	1.78	6.0E-04	AI862523.1	EST_HUMAN	w15a11.x1 NCI CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2402876 3'
4214	17243	30128	3.15	6.0E-04	U49563.1	NT	Homo sapiens CCR8 chemokine receptor (CMKR8) gene, complete cds
7830	20778	34156	0.59	6.0E-04	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0392
8198	21168		3.18	6.0E-04	P14608	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
8349	21318		0.69	6.0E-04	H82947.1	EST_HUMAN	y8a4c1.s1 Soares, pineal_gland_N3H3G Homo sapiens cDNA clone IMAGE:231666 3' similar to contains LOR1 repetitive element;
10339	23293		3.99	6.0E-04	ALD4807.2	EST_HUMAN	DKFZP568M2024.1 1 586 (synonym: luteal 1) Homo sapiens cDNA clone DKFZP568M2024
10440	23362	38852	2.19	6.0E-04	BE005860.1	EST_HUMAN	RC2-BN0120-250400-0121.h1 BN0120 Homo sapiens cDNA Lytechinus variegatus embryonic blastocoeilar extracellular matrix protein precursor (ECM3) mRNA, complete cds
10704	23626		0.65	6.0E-04	AF287478.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22 segment 2/3
11814	24699	38280	2.11	6.0E-04	AI225042.1	NT	U1H-B10-aab-09-03-J1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708925 3'
11893	24774	39360	3.12	6.0E-04	AW013847.1	EST_HUMAN	RC1-H10269-2811 99-012-408 HT0269 Homo sapiens cDNA
12384	25820		5.73	6.0E-04	AW380519.1	EST_HUMAN	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)
652	13718	26640	8.71	5.0E-04	O10341	SWISSPROT	QV0-CT0225-021098-030-a07 CT0225 Homo sapiens cDNA
1501	14834		1.88	5.0E-04	AW651844.1	EST_HUMAN	

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3424	16472	26391	1.28	5.0E-04	AA548931.1	EST_HUMAN	nk27ev1.1 s1 NCL CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element
3728	16770	26982	0.95	5.0E-04	Q9UKP4	SWISSPROT	ADAMTS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5549	18646	31588	2.37	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6784	19839	33124	6.64	5.0E-04	AA156080.1	EST_HUMAN	z033008.r1 Sitagliptin cdn (R637/204) Homo sapiens cDNA clone IMAGE:588953 5'
7602	20563	33924	10.72	5.0E-04	M23804.1	NT	Gorilla gorilla involucrin gene medium alkali, complete cds
8289	21259	34669	4.95	5.0E-04	A1188382.1	EST_HUMAN	q01308.x1 Soares_Platensis_20NHP869W Homo sapiens cDNA clone IMAGE:1723616 3' similar to gb:X51602_cde1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN) contains Alu repetitive element
8546	21614	35036	0.82	5.0E-04	AA814519.1	EST_HUMAN	0396d02.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339228 3' similar to contains element MER22 repetitive element
9032	22576	36026	1.57	5.0E-04	AA846546.1	EST_HUMAN	4156906.s1 Soares_Jettis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9726	22754	36207	0.62	5.0E-04	N83765.1	EST_HUMAN	KK2748F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2748 5' similar to REPETITIVE ELEMENT
9876	22829	36283	0.54	5.0E-04	P28126	SWISSPROT	BIJUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR
9963	22895	36338	4.56	5.0E-04	AIW270938.1	EST_HUMAN	x008d02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768853 3'
10640	23652		0.47	5.0E-04	U66871.1	NT	Human familial Alzheimer's disease (ST142) gene, complete cds
11320	24270		1.94	5.0E-04	AL048507.2	EST_HUMAN	DKFZ368M2024_j1 1885 (synonym: huter1) Homo sapiens cDNA clone DKFZ368M2024
12022	18546	31588	10.61	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12280	25763		4.4	5.0E-04	AA558513.1	EST_HUMAN	nf19f02.x1 NCL CGAP_Prl1 Homo sapiens cDNA clone IMAGE:913875
674	13738	26886	1.46	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
848	13904	26862	1.6	4.0E-04	A1720263.1	EST_HUMAN	aa70508.x1 Barstead cdn HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEINENYOL-COA HYDRATASE ;
848	13904	26863	1.6	4.0E-04	A1720263.1	EST_HUMAN	aa70508.x1 Barstead cdn HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEINENYOL-COA HYDRATASE ;
1451	14484	27486	2.78	4.0E-04	AIW753358.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENYOL-COA HYDRATASE ;
2095	15112	28133	1.57	4.0E-04	AL163278.2	NT	RC3-G10294-130100-023-001 C10294 Homo sapiens cDNA
2143	15160		0.99	4.0E-04	AL046704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
2635	15634	28658	1.66	4.0E-04	O96815	SWISSPROT	DKFZ434D059_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZ434D059 5'
3178	16233	29130	1.8	4.0E-04	AF281074.1	NT	SERPIN-2 (SILK GUM PROTEIN 2) Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4951	17378	30257	3.23	4.0E-04	AA576331.1	EST_HUMAN	h10a10.s1 NCL CGAP_Cot Homo sapiens cDNA clone IMAGE:591930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4951	17378	30258	3.23	4.0E-04	AA576331.1	EST_HUMAN	h10a10.s1 NCL CGAP_Cot Homo sapiens cDNA clone IMAGE:591930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4568	17591	30464	1.4	4.0E-04	AA086324.1	EST_HUMAN	zaf1g08.s1 Striatogene muscle 93/209 Homo sapiens cDNA clone IMAGE:562870 3'
5124	18133	31010	4.37	4.0E-04	BE560680.1	EST_HUMAN	601345595F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:3878910 5'
5288	18921		1.02	4.0E-04	AL163287.2	NT	Homo sapiens chromosome 21 segment HS210387
7483	20449	33806	1.26	4.0E-04	P48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7780	20733		0.78	4.0E-04	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
7987	20928	34321	0.98	4.0E-04	AU122078.1	EST_HUMAN	AUT122078 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
8881	21848	35289	1.07	4.0E-04	BF240712.1	EST_HUMAN	601876985F1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:4099700 5'
8889	21855	35275	1.56	4.0E-04	AI26507.1	EST_HUMAN	yc3b9t2.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:284142 5'
10049	22676	36442	3.11	4.0E-04	AI026693.1	EST_HUMAN	ov87f03.s1 Soares testis NIH Homo sapiens cDNA clone IMAGE:1843431 3'
10200	23125		1.11	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds
12694	25728		2.42	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
157	13260	26187	3.45	3.0E-04	AL119426.1	EST_HUMAN	DKFZp781J221.r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781J221 5'
197	13298	26228	1.95	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
881	13368	26895	1.64	3.0E-04	U83961.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1856	14882	27878	1.65	3.0E-04	AI282100.1	EST_HUMAN	q28d403.y1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1871	14968		1.43	3.0E-04	AI386674.1	EST_HUMAN	1f23a022.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2718082 3'
3319	16371	29291	3.17	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
3987	17027	29938	2.72	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4086	17120		1.21	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4120	17163		1.33	3.0E-04	BE140609.1	EST_HUMAN	RCOH-T0014-310596-028 HT0014 Homo sapiens cDNA
4854	17871		5.28	3.0E-04	BE163778.1	EST_HUMAN	PMO-HT0339-192000-007-g12 HT0339 Homo sapiens cDNA
5248	18255		1.02	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
6266	19339		5.73	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS210381
6993	20119	33432	1.92	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS210378
7183	18414	31216	0.71	3.0E-04	AI1683981.1	EST_HUMAN	RC4-NN0027-060403-011-b08 NN0027 Homo sapiens cDNA
7847	20794	34171	0.77	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8802	21570	34986	5.18	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
10280	23205	36689	1.44	3.0E-04	AA454055.1	EST_HUMAN	z48d06.r1 Soares testis NIH Homo sapiens cDNA clone IMAGE:78471 5' similar to gb:M62762 VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10538	23460	36957	0.58	3.0E-04	AI992139.1	EST_HUMAN	w75a11.x1 Soares_thymus_NHT Homo sapiens cDNA clone IMAGE:2513278 3'
10825	23746	37247	7.72	3.0E-04	AA781201.1	EST_HUMAN	q24g05.x1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M39072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
12245	25957	31315	3.98	3.0E-04	AA228301.1	EST_HUMAN	nc35a04.r1 NC1_CGAP_P2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L142 L1 repetitive element;
12623	25902	31525	5.33	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIA00749 protein, partial cds
13014	25504		4.33	3.0E-04	AL134483.1	EST_HUMAN	DKFZ5457L185 J1 947 (synonym: rfbt1) Homo sapiens cDNA clone DKFZp647L185 5'
177	13278	26204	1.29	2.0E-04	AF217796.1	NT	Homo sapiens SGG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
479	13551	26479	3.55	2.0E-04	AJ146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
908	13963	26919	4.01	2.0E-04	M86524.1	NT	Human dystrophin gene
908	13963	26920	4.01	2.0E-04	M86524.1	NT	Human dystrophin gene
1183	14224		2.52	2.0E-04	AJ269021.1	EST_HUMAN	q28a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
1190	14230		2.5	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1849	14875		1.19	2.0E-04	AF224388.1	NT	Mus musculus 5' flanking region of Pib3 gene
2194	15208		1.03	2.0E-04	AA478980.1	EST_HUMAN	Z1039005.g1 Soares_ovary_tumor_NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element
2381	15582	28601	4.05	2.0E-04	U68061.1	NT	Human gamine T-cell receptor beta chain TORBV1751A1T, TORBV231, TORBV10S1P, TORBV28S1P, TORBV18S1P, TORBV15S1, TORBV15S1A1T, HVB_refc, TORBV28S1P, TORBV34S1, TORBV14S1, TORBV35S1, TORBV45S1A1T, TR14, TR15, TR18, TR17, TR18, TORB1, TORB1S1, TORB1S2>
3000	16088	28677	1.13	2.0E-04	AJ124526.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3449	16486	28413	2.44	2.0E-04	BE082317.1	EST_HUMAN	QY2-BT0638-070500-194-b07 BT0638 Homo sapiens cDNA
3932	16972	28886	1.21	2.0E-04	AW978441.1	EST_HUMAN	EST359550 MAGE resequences, MAGEF Homo sapiens cDNA
4167	17198		5.41	2.0E-04	U01025.1	NT	Phascolus vulgaris nitrate reductase (PNR2) gene, complete cds
4686	17717	30812	1.21	2.0E-04	H68265.1	EST_HUMAN	y01e11.r1 Soares_pituitary_gland_NHPHG Homo sapiens cDNA clone IMAGE:232556 5'
4686	17717	30613	1.21	2.0E-04	H68265.1	EST_HUMAN	y01e11.r1 Soares_pituitary_gland_NHPHG Homo sapiens cDNA clone IMAGE:232556 5'
4834	17851		1.46	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5070	18080	30961	1.21	2.0E-04	H85683.1	EST_HUMAN	ys68b08.r1 Soares_retina_N2b4HR Homo sapiens cDNA clone IMAGE:218927 5' similar to contains L1 repetitive element;
5086	18108	30981	1.85	2.0E-04	AB037997.1	NT	Danio rerio tagoromo gene, exons 1 to 6, partial cds
5623	18719	31878	1.23	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCDU110 3'
5936	18732	31884	1.78	2.0E-04	AI890862.1	EST_HUMAN	tp03b011.x1 NC1_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207709 3'

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5843	19533	32117	1.15	2.0E-04	AA28652.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST1 containing O family repeat
6057	19138	33249	0.88	2.0E-04	4758179	NT	Homo sapiens cdi cycle progression 3 protein (DNJ3) mRNA
6098	19435	32678	0.8	2.0E-04	AF140708.1	NT	Homo sapiens G protein coupled receptor gene, complete cds; and unknown gene
7440	20407		2.54	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
7546	20309		0.51	2.0E-04	AW860663.1	EST_HUMAN	QV6-CT0387-180300-167-e10 CT0387 Homo sapiens cDNA
7882	20826		15.1	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7892	20835	34215	1.21	2.0E-04	P54286	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
8170	21109	34508	0.53	2.0E-04	AL043272.2	EST_HUMAN	DKFZp434L2023.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2023 5'
8170	21109	34509	0.53	2.0E-04	AL043272.2	EST_HUMAN	DKFZp434L2023.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2023 5'
8288	21257	34667	2.13	2.0E-04	U32444.2	NT	Scianum lycopersicum phytochrome F (PHYF) gene, partial cds
8288	21257	34668	2.13	2.0E-04	U32444.2	NT	Scianum lycopersicum phytochrome F (PHYF) gene, partial cds
8627	21595	35015	1.21	2.0E-04	AB026868.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8627	21595	35016	1.21	2.0E-04	AB026868.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8911	21877	35303	1.9	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
9095	22061	35486	0.56	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9689	22642	36100	0.51	2.0E-04	AA726700.1	EST_HUMAN	ar22a12 s1 Soares_testis_NHT Homo sapiens cDNA clone 1343518 3'
9774	22715	36170	0.65	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLOGF28.1
10334	23258	36735	1.21	2.0E-04	BE149303.1	EST_HUMAN	RC3H-IT0254-151099-011-b05 HT0254 Homo sapiens cDNA
10377	23300	36776	2.74	2.0E-04	AA405777.1	EST_HUMAN	z06c11.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742884 5'
11197	24152	37683	3.56	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA001 5'
11510	24451		2.59	2.0E-04	AJ243213.1	NT	Homo sapiens partial E-HT4 receptor gene, exons 2 to 5
11635	24572	38136	2.95	2.0E-04	AI440282.1	EST_HUMAN	U10111.x1 NCI_CGAP_Gae4 Homo sapiens cDNA clone IMAGE:2140260 3' similar to contains Alu repetitive element
11755	24683	38262	2.49	2.0E-04	AW136740.1	EST_HUMAN	U1-H-B1-adm-c-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
768	13927	26771	0.81	1.0E-04	H98646.1	EST_HUMAN	w26c09.s1 Soares_melanocyte_2NDHM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.11 repetitive element
951	14004	26956	2.03	1.0E-04	P48725	SWISSPROT	PERCENTRIN
1076	14121	27072	2.61	1.0E-04	P11969	SWISSPROT	RETROVIRUS RELATED POLYPROTEIN [CONTAINS; REVERSE TRANSCRIPTASE; ; ENDONUCLEASE]
1116	14160	27110	4.21	1.0E-04	AW013947.1	EST_HUMAN	U1-H-B10-aab-e-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'

### Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1116	14160	27111	4.21	1.0E-04	AW013847.1	EST_HUMAN	U1-H3C- <i>ad</i> -v-09-0-U1.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708826 3'
1335	14369		3.08	1.0E-04	U62918.1	NT	Angiella anguilla dopamine DAT1 receptor (DAT1) gene, complete cds
1632	14665	27840	3.19	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1632	14665		3.19	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1878	14903	27903	2.37	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
2668	16064	28710	1.06	1.0E-04	BE218833.1	EST_HUMAN	h45608.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176368 3'
2668	16064	28711	1.05	1.0E-04	BE218833.1	EST_HUMAN	h45608.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176368 3'
3267	16350	28270	1.14	1.0E-04	Q62203	SWISSPROT	SPUCEOSOME ASSOCIATED PROTEIN 62 (GAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3748	16780	29702	0.83	1.0E-04	AI440282.1	EST_HUMAN	g0111.x1 NCL CGAP_Gae4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element
4089	17123	30017	2.07	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4109	17149	30037	1.04	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBDD04 3'
5132	18141	31019	1.87	1.0E-04	7682015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5132	18141	31020	1.87	1.0E-04	7682015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5137	18146	31026	0.92	1.0E-04	AI337156.1	EST_HUMAN	q62604.x1 NCL CGAP_GCA Homo sapiens cDNA clone IMAGE:2006675 3'
5980	19045	32244	1.19	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6033	19116	32319	0.32	1.0E-04	T19815.1	EST_HUMAN	733F Heart Homo sapiens cDNA clone 733
6033	19116	32320	0.32	1.0E-04	T19815.1	EST_HUMAN	733F Heart Homo sapiens cDNA clone 733
8579	19639	32605	0.9	1.0E-04	AA177111.1	EST_HUMAN	np02e12.s1 NCL CGAP_P33 Homo sapiens cDNA clone IMAGE:252
7012	20138	33455	0.66	1.0E-04	AA564561.1	EST_HUMAN	U125604.s1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:993486 3' similar to gb:M97282
7392	20361	33713	12.86	1.0E-04	AI251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element
7821	20381	33713	12.73	1.0E-04	AI251980.1	EST_HUMAN	q47610.x1 NCL CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
8328	21287	34712	0.59	1.0E-04	AA630453.1	EST_HUMAN	q57610.x1 NCL CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
9662	22645	36102	0.88	1.0E-04	AI806220.1	EST_HUMAN	ab94p08.s1 Stragene lung (h837210) Homo sapiens cDNA clone IMAGE:854654 3'
9703	22656	36111	1.47	1.0E-04	O88869	SWISSPROT	w26008.x1 Sources: NFI_T_GBC S17 Homo sapiens cDNA clone IMAGE:2369742 3'
9780	22721		0.83	1.0E-04	T77163.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 6)
10004	22931	36394	1.89	1.0E-04	10883878	NT	y172608.r1 Sources fetal liver spleen 1MFLS1 Homo sapiens cDNA clone IMAGE:11374 5'
10539	23461		0.91	1.0E-04	P08547	SWISSPROT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10578	23468	36960	0.91	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11567	24603		1.74	1.0E-04	M25987.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11561	24840	38403	1.5	1.0E-04	AB032968.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
11599	24876	38472	1.48	1.0E-04	AW260061.1	EST_HUMAN	xif6g12.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
12032	24808	38602	1.81	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12032	24808	38503	1.81	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12413	25770		2.4	1.0E-04	BE576398.1	EST_HUMAN	7129a10.x1 NCL_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:3268658 3' similar to contains L1.13 L1
13061	25697		1.38	1.0E-04	BE700353.1	EST_HUMAN	repetitive element;
689	13761	26683	2.39	1.0E-05	AA718933.1	EST_HUMAN	PMMA-NN0091-190700-004-F11 NN0091 Homo sapiens cDNA
2020	15041	28052	1.09	9.0E-05	AA718933.1	EST_HUMAN	QV4-SN0023-070400-166-B04 SN0023 Homo sapiens cDNA
6074	19155	32367	1.58	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7528	20776	34453	0.67	9.0E-05	AW204958.1	EST_HUMAN	UI-H-B1-ae-4-05-0-J1 st NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
7528	20776	34154	0.67	9.0E-05	AW204958.1	EST_HUMAN	UI-H-B1-ae-4-05-0-J1 st NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9831	22680		2.89	9.0E-05	D65606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
9833	22682	36137	3.13	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11472	24415	37584	2.03	9.0E-05	AW073078.1	EST_HUMAN	repetitive element;
11938	19155	32367	3.21	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12465	25832		3.02	9.0E-05	AF128756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DD4H, G6b, G8c, G8d, G8e, G8f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
822	13880	26831	1.79	8.0E-05	AJ251646.1	NT	Plum sativum mRNA for beta-1,3 glucanase (gms2 gene)
865	13921		7.38	8.0E-05	AJ251646.1	NT	Plum sativum mRNA for beta-1,3 glucanase (gms2 gene)
2891	18019		0.91	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4507	17532	30415	0.87	8.0E-05	AW044605.1	EST_HUMAN	wy78d04.xt Soares_NSIF_FB_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
6101	22067	35463	0.48	8.0E-05	Y11666.1	NT	Mus musculus gene for hexokinase II, exon 1 (end joined CDS)
11485	24428	37979	3.06	8.0E-05	M65167.1	NT	Human lactoglobulin and lactoglobulin-related protein (HP and HPR) genes, complete cds
13050	25815		2.74	8.0E-05	AA276333.1	EST_HUMAN	z88h01 st NCL_CGAP_QCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu
347	13436	26358	6.11	7.0E-05	AW847445.1	EST_HUMAN	repetitive element; contains element MSK1 repetitive element;
347	13436	26359	8.11	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220398-011-E04 CT0208 Homo sapiens cDNA
569	13039	26553	1	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human foetal cDNA Homo sapiens cDNA clone EST HFD072014
569	13039	26554	1	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human foetal cDNA Homo sapiens cDNA clone EST HFD072014

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1058	14104	27055	1.47	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYL TRANSFERASE, MITOCHONDRIAL PRECURSOR (OPAT)
2730	15724	28740	4.26	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3172	18227	29143	4.21	7.0E-05	AB009480.1	NT	Dicystellum discoidium gene for TRFA, complete cds
3714	18757		0.9	7.0E-05	AI432413.1	EST_HUMAN	bt3509.x1 Scars. NIH/PU S1 Homo sapiens cDNA clone IMAGE:2114418 3'
4400	17428	30313	1.53	7.0E-05	AL15201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4982	17977	30857	0.69	7.0E-05	9845300	NT	Rat cyclomarginatus Maelstrom, complete genome
8567	21535	34955	1.27	7.0E-05	AA505582.1	EST_HUMAN	nh8301.g1 NCI CGAP B12 Homo sapiens cDNA clone IMAGE:86608 3'
9611	22732	36187	3.34	7.0E-05	U07095.1	EST_HUMAN	EST04984 Fetal brain, Stratiene (cat835206) Homo sapiens cDNA clone HFBED60
10982	23802	37415	0.44	7.0E-05	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
10982	25902	37416	0.44	7.0E-05	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
11465	24438		9	7.0E-05	10355048	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2041	15050	28080	1.6	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
2041	15050	28081	1.6	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
2594	15595	28613	1.05	6.0E-05	AI655241.1	EST_HUMAN	wo54h06.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gbJ03250 DNA
2694	16590	28707	1.3	6.0E-05	Z84506.1	NT	TOPOISOMERASE I (HUMAN);
2694	16590	28708	1.3	6.0E-05	Z84506.1	NT	H sapiens flow-sorted chromosome 6 HindIII fragment, SC8pA28B 10
2825	13743	29669	3.23	6.0E-05	AF053830.1	NT	H sapiens flow-sorted chromosome 6 HindIII fragment, SC8pA28B 10
5107	18117	30980	0.93	6.0E-05	AV722942.1	EST_HUMAN	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5107	18117	30991	0.93	6.0E-05	AV722942.1	EST_HUMAN	AV722942.H18 Homo sapiens cDNA clone HTBBED12 5'
8019	19102	32303	3.06	6.0E-05	Q12960	SWISSPROT	AV722942.H18 Homo sapiens cDNA clone HTBBED12 5'
8019	19102	32304	3.06	6.0E-05	Q12960	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP195)
8543	19605	32867	1.45	6.0E-05	N72829.1	EST_HUMAN	CONTACTIN PRECURSOR (GLYCOPROTEIN GP195)
7119	20053	33337	0.77	6.0E-05	AA897890.1	EST_HUMAN	YF001711 Scars. fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:246212 5'
8421	21390	34600	0.71	6.0E-05	BE004410.1	EST_HUMAN	q80403.g1 Scars. NFL T. GBC S1 Homo sapiens cDNA clone IMAGE:1904588 3'
8421	21390	34601	0.71	6.0E-05	BE004410.1	EST_HUMAN	RC4-BT0311-141189-01-H08 BT0311 Homo sapiens cDNA
8786	21753	35175	0.68	6.0E-05	AA150482.1	EST_HUMAN	RC4-BT0311-141189-01-H08 BT0311 Homo sapiens cDNA
8791	21758	35180	2.37	6.0E-05	AA150482.1	EST_HUMAN	contains element MER28 repetitive element;
8927	21893	35321	0.61	6.0E-05	Q80401	SWISSPROT	PM4-NN0050-310300-001-110 NN0050 Homo sapiens cDNA
9807	22611	36083	1.11	6.0E-05	P08607	SWISSPROT	COMPLEMENT DECA-ACCELERATING FACTOR PRECURSOR
9807	22611	36084	1.11	6.0E-05	P08607	SWISSPROT	CAB-BINDING PROTEIN PRECURSOR (C4BP)
9879	22832	36286	1.05	6.0E-05	T94149.1	EST_HUMAN	CAB-BINDING PROTEIN PRECURSOR (C4BP) y82b12.11 Stratiene lung (#837210) Homo sapiens cDNA clone IMAGE:110062 5'



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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10079	23006	36477	0.71	6.0E-05	AW627065.1	EST_HUMAN	h37a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874444 3'
11100	24090	37584	2.27	6.0E-05	R75639.1	EST_HUMAN	y65003.s1 Soares placenta N22-IP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains L1R1 repetitive element ;
11847	24730	38316	2.71	6.0E-05	AA044015.1	EST_HUMAN	zk5802.7 Soares_pregnant_uterus_NbriPU Homo sapiens cDNA clone IMAGE:487035 5'
12670	23513	31529	16.08	6.0E-05	AV880110.1	EST_HUMAN	MRO-NT0038-250400-001-109 NT0038 Homo sapiens cDNA
1403	14436	27404	16.34	5.0E-05	AV392088.1	EST_HUMAN	OYA-ST0234-241189-040-111 ST0234 Homo sapiens cDNA
1880	14805		1.15	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC558595), mRNA
4004	17043	29951	3.54	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5603	16599	31670	11.74	5.0E-05	X58555.1	NT	Human MLC1 gene for embryonic myosin alkaline light chain, 3'UTR
6107	19186	32405	3.22	5.0E-05	AV563544.1	EST_HUMAN	AV563544 GLC Homo sapiens cDNA clone GLC/DMA06 3'
8282	19384	32603	0.84	5.0E-05	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7353	20516		1.18	5.0E-05	AB037854.1	NT	Mus musculus gene for calretinin, exon 1
12462	25371		5.88	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12717	25371		4.8	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2818	13329		4.95	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
4508	17533	30418	1.88	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4508	17533	30417	1.88	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4910	17827		0.99	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
7127	20060	33366	0.71	4.0E-05	U01947.1	NT	Macaca mulatta lactoglobulin (HP) gene, 5' region
8881	22834		8.43	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
10360	23283	36760	0.51	4.0E-05	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
10771	25692	37189	0.66	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
11120	24080	37604	3.91	4.0E-05	AW627046.1	EST_HUMAN	h38a07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element ;
12423	25182		2.48	4.0E-05	AW117580.1	EST_HUMAN	x63609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805182 3'
13081	25612		2.29	4.0E-05	AA417756.1	EST_HUMAN	q184c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:748252 3'
681	13744	26671	0.78	3.0E-05	AI249061.1	EST_HUMAN	q184c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:748252 3'
1061	14107	27057	1.89	3.0E-05	AW273851.1	EST_HUMAN	x24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1133	14176	27125	0.82	3.0E-05	BF037888.1	EST_HUMAN	601461463F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3865142 5'
1133	14176	27126	0.82	3.0E-05	BF037888.1	EST_HUMAN	601461463F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3865142 5'
4408	17437	30324	8.15	3.0E-05	BE186211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4409	17437	30325	8.15	3.0E-05	BE186211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4493	17518	30405	2.41	3.0E-05	AA388879.1	EST_HUMAN	EST79998 Plectra1 Homo sapiens cDNA similar to p53-associated protein
4493	17518	30406	2.41	3.0E-05	AA388879.1	EST_HUMAN	EST79998 Plectra1 Homo sapiens cDNA similar to p53-associated protein
4820	17541		0.7	3.0E-05	AL193302.2	NT	Homo sapiens chromosome 21 segment HS21C102
5837	18733	31895	1.78	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (MyLC2pl), mRNA
6921	19871	33287	1.18	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6921	19871	33288	1.18	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8290	21198	34608	2.48	3.0E-05	BE733157.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842932 5'
8893	21683	35087	1.88	3.0E-05	AA284049.1	EST_HUMAN	3260505.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8244	22210	35641	1.54	3.0E-05	AW770982.1	EST_HUMAN	H84608.x1 NC1_CGAP_L102 Homo sapiens cDNA clone IMAGE:3009693 3'
9248	22214	35644	1.37	3.0E-05		NT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9252	22218	35649	0.59	3.0E-05	P43351	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-9 ANTIGEN)
9486	22450		0.51	3.0E-05	X03273.1	NT	Human A1u-family cluster 5' of alpha(1)-acid glycoprotein gene
9675	22628	35081	1.2	3.0E-05	AA372562.1	EST_HUMAN	EST84475 Caten adenocarcinoma IV Homo sapiens cDNA 5' end
10021	22948		3.24	3.0E-05	AJ769337.1	EST_HUMAN	wg58009.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10801	23821	37330	0.89	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
10801	23821	37331	0.89	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
12343	25147		1.49	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
2332	15343	28385	1.32	2.0E-05	AI286021.1	EST_HUMAN	q199611.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:1856552 3' similar to contains MERK3 repetitive element ;
2587	15988	28605	2.2	2.0E-05	M13792.1	NT	Human adenocarcinoma desminase (ADA) gene, complete cds
2725	15719		7.98	2.0E-05	AA1160502.1	EST_HUMAN	zz484812.r1 Stralagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains A1u repetitive element contains element L1 repetitive element ;
3154	18211	29126	1.15	2.0E-05	BC086038.1	EST_HUMAN	RC3-BT0319-120200-014-08 BT0319 Homo sapiens cDNA
3359	18409	29331	0.88	2.0E-05	AF194614.1	NT	Homo sapiens p27-phox (NCF1) gene, complete cds
3382	18431	28339	1.35	2.0E-05	X99211.1	NT	H.sapiens DNA for endogenous retroviral like element
3505	18552		0.7	2.0E-05	X95465.1	NT	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3920	16880		0.69	2.0E-05	AJ339107.1	EST_HUMAN	DKFZc5681084.11 568 (synonym: hfk2) Homo sapiens cDNA clone DKFZc5681084 5'
4720	17740		1	2.0E-05	BC378471.1	EST_HUMAN	601268455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3008653 5'
5852	18943	32128	1.57	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (end joined CDS)
6024	19107		0.65	2.0E-05	AF026308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
6082	19182	32373	0.86	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA+)/DICARBOXYLATE COTRANSPORTER)

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
6082	19162	32374	0.86	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6281	19553	32589	0.88	2.0E-05	A149272.1	EST_HUMAN	q672a02.x1 Soares_placenta_Bio8weeks_2NhpP8tc9w Homo sapiens cDNA clone IMAGE:1715114 3' similar to contains L1.13 L1 repetitive element
6356	19425	32657	0.49	2.0E-05	P35085	SWISSPROT	CALCIUM-BINDING PROTEIN
6778	19833	33116	2.32	2.0E-05	A4714330.1	EST_HUMAN	iw06012.s1 NCI CGAP_SST Homo sapiens cDNA clone IMAGE:1238519 3'
7085	20020	33322	1.52	2.0E-05	P08926.1	NT	P14ciparum mRNA for IARF1 protein, partial
7099	20033	33336	0.84	2.0E-05	A1492960.1	EST_HUMAN	Q02711 PRO-POL-DUTPASE POLYPROTEIN
7108	20042		8.82	2.0E-05	A1991025.1	EST_HUMAN	w035h07.x1 Soares_Dickgreife_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7390	20330	33879	2.22	2.0E-05	AF224282.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), and HoxA1 (HoxA1) genes, complete cds
7390	20330	33680	2.22	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), and HoxA1 (HoxA1) genes, complete cds
7562	20553		0.81	2.0E-05	AF128847.1	NT	Homo sapiens inducible Myeloblastin N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
8157	21095	34494	0.5	2.0E-05	U69051.1	NT	Human germine T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV1HS1A1T, HV8 ralle, TCRBV29S1P, TCRBV24S1P, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRB11S1, TCRB11S2>
8217	21166	34586	1.25	2.0E-05	A831040.1	EST_HUMAN	h22h05.x1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
9477	22441	35681	0.52	2.0E-05	BE244840.1	EST_HUMAN	TGAP2J1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCSA Homo sapiens cDNA clone TCSAP1590
9477	22441	35682	0.52	2.0E-05	BE244840.1	EST_HUMAN	TCSAP2J1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCSA Homo sapiens cDNA clone TCSAP1590
9822	22566	36015	0.57	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9822	22566	36016	0.57	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10283	23208	36693	0.87	2.0E-05	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10494	23416	36914	0.87	2.0E-05	BF655939.1	EST_HUMAN	7755g08.y1 NCI CGAP_Brn20 Homo sapiens cDNA clone IMAGE:3340576 5'
10954	23874	37387	2.1	2.0E-05	N41751.1	EST_HUMAN	iw01a06.r1 Soares_placenta_Bio8weeks_2NhpP8tc9w Homo sapiens cDNA clone IMAGE:259570 5'
10954	23874	37388	2.1	2.0E-05	N41751.1	EST_HUMAN	iw01a06.r1 Soares_placenta_Bio8weeks_2NhpP8tc9w Homo sapiens cDNA clone IMAGE:259570 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11006	20042		2.01	2.0E-05	AI961026.1	EST_HUMAN	Wt3507.x1 Soares, Dieckgrafe colon, NHCD Homo sapiens cDNA clone IMAGE:2520777 3'
11781	23936	37457	1.9	2.0E-05	BE176801.1	EST_HUMAN	RC5b.HT0582:280300-012-E12:HT0582 Homo sapiens cDNA
12473	25740		6.5	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Ki671 Homo sapiens cDNA clone IMAGE:3189532 3' similar to TR-Q12832
12626	25727		1.54	2.0E-05	AF275948.1	NT	Q12932 GLYCOPHORIN HEP2;
12766	25408	31759	1.49	2.0E-05	AI131513.1	EST_HUMAN	Homo sapiens ABCA1 (ABCA1) gene, complete cds
1705	15902	28715	3.2	1.0E-05	AL163282.2	EST_HUMAN	AIU131513.NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
3603	16706	29821	1.86	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lamt0 120 Suppressor of Hairless (Su(H)) gene, partial cds
3626	18666		1.17	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3981	17031	25940	10.43	1.0E-05	P61274	SWISSPROT	MOSAIC PROTEIN LGN
4201	17232	30119	1.52	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4306	17335	30213	1.77	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.t1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:781494 5'
4887	17904	30783	1.82	1.0E-05	AW418134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2956548 3'
5005	18019	30907	0.94	1.0E-05	Z18943.1	NT	H. sapiens repeat region
6015	19987	33262	1.03	1.0E-05	AJ246003.1	NT	Homo sapiens Spad gene for spastin protein
7028	18360	31251	0.52	1.0E-05	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7286	20663	33370	3.02	1.0E-05	AA641846.1	EST_HUMAN	ns1902.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.1 L1
7288	20260	33594	8.81	1.0E-05	4505844	NT	L1 repetitive element;
							Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7921	20894	34252	0.66	1.0E-05	BF222846.1	EST_HUMAN	7a57d01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3648945 3' similar to contains MER10.B3
8057	20994		1.3	1.0E-05	P19474	SWISSPROT	MER10 repetitive element;
9266	22232		2.45	1.0E-05	AL163227.2	NT	52 KD RD PROTEIN (S)OGEN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SA-A))
							Homo sapiens chromosome 21 segment HS21C027
9415	22380	35818	2.22	1.0E-05	AA452578.1	EST_HUMAN	z33h12.s1 Soares, testis, Nht2-HF8, 9w Homo sapiens cDNA clone IMAGE:788519 3' similar to
							gbL102932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9642	22586	36035	14.03	1.0E-05	AA236110.1	EST_HUMAN	z40841.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:864332 5' similar to contains Alu
9721	22749	36201	0.82	1.0E-05	AW732160.1	EST_HUMAN	repetitive element contains element TART1 repetitive element;
							AF732160.HTF Homo sapiens cDNA clone HTFBH07 5'
10198	23123	36809	0.79	1.0E-05	AW510902.1	EST_HUMAN	ORF11 OFR repetitive element;
							h441b02.x1 Soares, NFI_L_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812043 3' similar to contains
10198	23123	36810	0.79	1.0E-05	AW510902.1	EST_HUMAN	ORF11 OFR repetitive element;
10276	23201	36885	1.11	1.0E-05	AW291521.1	EST_HUMAN	UHF-B12-agk-a-08-c-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724389 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10276	23201	36686	1.11	1.0E-05	AW281521.1	EST_HUMAN	U1-H-B12-agk-a-08-0-U1.x1 NC1_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724393 3'
10544	23466		1.95	1.0E-05	AW465995.1	EST_HUMAN	h07c10.x1 NC1_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2673010 3' similar to contains L1 L2 L1 repetitive element;
11264	24216	37740	1.79	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11264	24216	37741	1.79	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12841	25600	31421	1.43	1.0E-05	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2680	15676	28597	5.9	9.0E-06	AI583811.1	EST_HUMAN	tt73a06.x1 NC1_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246366 3'
3112	16169	29079	4.25	9.0E-06	AI218983.1	EST_HUMAN	qq11503.x1 Scars_placenta_8169weeks_2NH8P8160W Homo sapiens cDNA clone IMAGE:1759191 3'
3624	15687		2.82	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6008	19091	32291	2.31	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
7047	20069	33375	0.73	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-407 BT0313 Homo sapiens cDNA
7674	20632	33696	0.94	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8053	20980	34388	11.84	9.0E-06	AI034370.1	EST_HUMAN	alpha2p01.x1 Scars_fetal_liver_spleen_1NRLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element
8807	21774	35200	1.18	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9334	22299	35728	2.51	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V.SRC)
9334	22299	35729	2.51	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V.SRC)
9577	22539	35990	4.44	9.0E-06	U35714.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11295	24236	37703	3.65	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C32E12.14C
2535	19896	28559	2.63	8.0E-06	AW362539.1	EST_HUMAN	RCS-C70283-201199-011-H11_C70283 Homo sapiens cDNA
10898	23818	37326	0.64	9.0E-06	P24083	SWISSPROT	FASCDILIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10898	23818	37327	0.54	9.0E-06	P24083	SWISSPROT	FASCDILIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
980	14031		2.14	7.0E-06	AA698729.1	EST_HUMAN	ab09f10.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.1 MER20 repetitive element;
1433	14467	27444	3.05	7.0E-06	7692177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2884	15943		7.94	7.0E-06	AI368352.1	EST_HUMAN	qpr18g09.x1 NC1_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element.

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Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3576	16821		0.78	7.0E-06	AA385542.1	EST_HUMAN	EST162626 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5760	18872		5.19	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0082 Thyroid Homo sapiens cDNA
5902	18893	32179	0.81	7.0E-06	N98845.1	EST_HUMAN	Y65C07.r1 Scores_multiple_sclerosis_2N3HMSF Homo sapiens cDNA clone IMAGE:278412 5'
9141	22107	35533	0.7	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (G31 gene) (DXF6851E), mRNA
10260	23185		0.54	7.0E-06	Q31147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXYDASE)
12202	25927	31307	2.83	7.0E-06	BF215672.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5'
2228	15966	26907	1.27	6.0E-06	BE09168.1	EST_HUMAN	QV2-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
3708	18749	28684	1.08	6.0E-06	BE069186.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
4785	16010	28938	2.35	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4794	17811	30703	2.54	6.0E-06	A1040998.1	EST_HUMAN	cd082.x1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.2 MER8 repetitive element.
5422	18525	31403	1.41	6.0E-06	AF167441.1	EST_HUMAN	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5483	19583	31496	1.05	6.0E-06	Q02040	SWISSPROT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
10215	23140		1.52	6.0E-06	AW801812.1	EST_HUMAN	IL5-UM0070-0-110400-065-002 UM0070 Homo sapiens cDNA
13041	25582	31700	1.74	6.0E-06	11418167	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
6179	18254	32487	3.86	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6471	19536	32784	3.96	5.0E-06	U075961.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7444	20410	33762	1.14	5.0E-06	AB007546.1	NT	Human CTG1302-120200-013-102 CT1302 complete cds
8803	21770	35195	0.49	5.0E-06	AW555672.1	EST_HUMAN	RC1-CT1302-120200-013-102 CT1302 Homo sapiens cDNA
8803	21770	35196	0.48	5.0E-06	AW555672.1	EST_HUMAN	RC1-CT1302-120200-013-102 CT1302 Homo sapiens cDNA
10462	23384	36877	7.1	5.0E-06	AA333620.1	EST_HUMAN	EST185498 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
12101	24972	38599	2	5.0E-06	Q28039	SWISSPROT	SODIUM- AND CHLORIDE-DEPENDENT GLYCINE TRANSPORTER 1 (GLYT-1)
12828	25512	31709	2.14	5.0E-06	A105045.1	EST_HUMAN	HA0377 Human fetal liver cDNA library Homo sapiens cDNA
648	13714	26835	8.59	4.0E-06	R18287.1	EST_HUMAN	ye48033 J1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains ALU repetitive element/contains L1 repetitive element.
847	13903	26861	6.33	4.0E-06	AW103354.1	EST_HUMAN	xc63912.x1 NCI CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains ALU repetitive element/contains element MER21 repetitive element.
1337	14371	27340	4.22	4.0E-06	A1334928.1	EST_HUMAN	h334909.x1 NCI CGAP_HSC27 Homo sapiens cDNA clone IMAGE:2056168 3'
1337	14371	27341	4.22	4.0E-06	A1334928.1	EST_HUMAN	h334909.x1 NCI CGAP_HSC27 Homo sapiens cDNA clone IMAGE:2056168 3'
1470	14503	27477	2.58	4.0E-06	BF366612	EST_HUMAN	QV2-NT0046-209060-250-007 NT0046 Homo sapiens cDNA
2274	15287	28313	3.05	4.0E-06	AW015401.1	EST_HUMAN	U1H-B10-aet1-045-0J1 at NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2770425 3'
3076	16133	29046	0.94	4.0E-06	AF1488349.1	NT	Gallus gallus Dact2 protein (Dact2), mRNA, complete cds

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3909	16949	29860	1.1	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4946	17683	30756	2.18	4.0E-06	AB895939.1	EST_HUMAN	WIG410.X1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element.
8344	21811	35230	0.55	4.0E-06	C15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
8152	22118	35545	3.3	4.0E-06	AF009600.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
10066	22983	36462	1.14	4.0E-06	AJ272365.1	NT	Homo sapiens SP22 gene for secreted phosphoprotein 24 precursor, exons 1-8
11778	23833	37454	2.91	4.0E-06	AB007955.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIA0488
2173	15189	28209	1.9	3.0E-06	AA700562.1	EST_HUMAN	Z34308.s1 Soares, fetal_liver_spleen, 1N1FLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element.
2173	15189	28210	1.9	3.0E-06	AA700562.1	EST_HUMAN	Z34308.s1 Soares, fetal_liver_spleen, 1N1FLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element.
2275	15288		1.89	3.0E-06	AF202635.1	NT	Homo sapiens PPT200 mRNA, complete cds
2833	15891	28911	0.95	3.0E-06	AA868218.1	EST_HUMAN	sk48g11.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains L1.TR1.13 L1T1 repetitive element.
3278	16333		2.32	3.0E-06	AB57776.1	EST_HUMAN	W22805.X1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR-O60734 O60734 LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element.
3787	16837	29743	1.12	3.0E-06	BE047094.1	EST_HUMAN	hg44412.X1 NCI CGAP_HNT3 Homo sapiens cDNA clone IMAGE:3124161 3'
3797	16837	29744	1.12	3.0E-06	BE047094.1	EST_HUMAN	hg44412.X1 NCI CGAP_HNT3 Homo sapiens cDNA clone IMAGE:3124161 3'
4501	17526	30411	0.67	3.0E-06	T50266.1	EST_HUMAN	x678b10.r1 Stratogene ovary (4637/217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4594	17615	30509	4.02	3.0E-06	X64816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus).
6284	19356	32592	0.74	3.0E-06	AU169412.1	EST_HUMAN	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
6974	20197	33525	0.56	3.0E-06	Z79478.1	NT	H. sapiens flow-sorted chromosome 6 Tail fragment, SC6pA9E5
6974	20197	33526	0.56	3.0E-06	Z79478.1	NT	H. sapiens flow-sorted chromosome 6 Tail fragment, SC6pA9E5
7439	20406		1.9	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8418	21398	34798	0.76	3.0E-06	BE652694.1	EST_HUMAN	301396231.F1 NIH/MGC_44 Homo sapiens cDNA clone IMAGE:3680314 5'
9032	21998	35417	0.64	3.0E-06	P07743	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
12631	25317		6.4	3.0E-06	AW395282.1	EST_HUMAN	RG0-L10001-281195-011-A03 LT0001 Homo sapiens cDNA
203	13304		3.24	2.0E-06	P54366	SWISSPROT	HOMEBOX PROTEIN GOOSECOID
1572	14605		5.6	2.0E-06	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE, REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2387	15385	28420	2.64	2.0E-06	AI672138.1	EST_HUMAN	w640403.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2267068 3' similar to contains MER30.b1 MER30 repetitive element.
2474	15478	28501	2.73	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2573	15574	28594	1.84	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3331	16577	29500	1.29	2.0E-06	AV857655.1	EST_HUMAN	AV857655 GLC Homo sapiens cDNA clone GLC08053'
3774	16818	29725	1.86	2.0E-06	AA173518.1	EST_HUMAN	zfp2605.11 Strabegov ovarian cancer (#637219) Homo sapiens cDNA clone IMAGE:569332 5'
3783	16824	29732	0.87	2.0E-06	AW450215.1	EST_HUMAN	ULH-B3-alky-g-05-AJ1.51 NCI_CGAP_S405 Homo sapiens cDNA clone IMAGE:2736170 3'
3789	16830	29736	1.74	2.0E-06	AB030886.1	NT	Mus musculus gene for odorant receptor A18, complete cds
6208	19282		0.9	2.0E-06	AA974932.1	EST_HUMAN	on34h01 s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:158606 3' similar to contains Alu repetitive element
6241	19314	32544	0.93	2.0E-06	AI539448.1	EST_HUMAN	hs105.41 Soares_NFL_T_GRC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR-Q13537
6581	19841	32908	5.37	2.0E-06	AI819424.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE .
8250	21219		0.81	2.0E-06	AW869223.1	EST_HUMAN	WJ93004.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410683 3'
8426	21395	34806	0.83	2.0E-06	T12238.1	EST_HUMAN	MR3-SND087-1200-002-002 SN0087 Homo sapiens cDNA
9188	22154		0.81	2.0E-06	AA172497.1	EST_HUMAN	A4478 Heart Homo sapiens cDNA clone A447
9200	22166	35596	1.83	2.0E-06	H62051.1	EST_HUMAN	z127c11 s1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to
9571	22533	35883	0.87	2.0E-06	AF003529.1	NT	TRP70467 P70467 REVERSE TRANSCRIPTASE .
9571	22533	35884	0.97	2.0E-06	AF003529.1	NT	X37604.11 Soares ovary tumor N3HOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74029
9591	22553		0.48	2.0E-06	AA173450.1	EST_HUMAN	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
10059	22986	36454	0.92	2.0E-06	N30576.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10279	23204		0.61	2.0E-06	AV748968.1	EST_HUMAN	Human glypican 3 (GPC3) gene, partial cds and flanking repeat regions
12111	24081	36581	2.21	2.0E-06	O15563	SWISSPROT	Human glypican 3 (GPC3) gene, partial cds and flanking repeat regions
12111	24081	36582	2.21	2.0E-06	O15563	SWISSPROT	Human glypican 3 (GPC3) gene, partial cds and flanking repeat regions
12540	25028	31308	2.97	2.0E-06	P23249	SWISSPROT	Human glypican 3 (GPC3) gene, partial cds and flanking repeat regions
13659	25986	36454	0.92	2.0E-06	N30576.1	EST_HUMAN	Human glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10279	23204		0.61	2.0E-06	AV748968.1	EST_HUMAN	Human glypican 3 (GPC3) gene, partial cds and flanking repeat regions
12111	24081	36581	2.21	2.0E-06	O15563	SWISSPROT	Human glypican 3 (GPC3) gene, partial cds and flanking repeat regions
12111	24081	36582	2.21	2.0E-06	O15563	SWISSPROT	Human glypican 3 (GPC3) gene, partial cds and flanking repeat regions
12540	25028	31308	2.97	2.0E-06	P23249	SWISSPROT	Human glypican 3 (GPC3) gene, partial cds and flanking repeat regions
36	13156	26057	3.02	1.0E-06	AF076082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
658	13724	26949	1.96	1.0E-06	AF084354.1	NT	Mus musculus D6MME protein (D6MME) mRNA, complete cds
1445	14478	27454	1.81	1.0E-06	P09125	SWISSPROT	MERCZOTIE SURFACE PROTEIN CAZ-8
1527	14580	27531	1.87	1.0E-06	AL163278.2	NT	Homo sapiens chromosome 21 segment H6210078
1576	14609	27582	1.22	1.0E-06	AA034141.1	EST_HUMAN	z06a12 s1 Soares_fetal_liver_apical_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to contains Alu repetitive element;
1576	14609	27583	1.22	1.0E-06	AA034141.1	EST_HUMAN	z06a12 s1 Soares_fetal_liver_apical_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to contains Alu repetitive element;



Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1587	14620		1.38	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2010	15031	28040	5.53	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2010	15031	28041	5.53	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4397	17425	30309	13.21	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5146	18155	31034	1.23	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5146	18155	31035	1.23	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5383	18468	31339	4.63	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT10800-030700-002-c06 B T0800 Homo sapiens cDNA
5388	18481	31387	1.01	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090900-001-c04 FN0004 Homo sapiens cDNA
5388	18491	31388	1.01	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090900-001-c04 FN0004 Homo sapiens cDNA
5552	18849	31592	1.24	1.0E-06	O60613	SWISSPROT	15 KDA SEL ENOPROTEIN PRECURSOR
5952	18960		0.64	1.0E-06	BE063527.1	EST_HUMAN	CMO-BT0281-031199-087-004 BT0281 Homo sapiens cDNA
7056	20078	33387	6.4	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA1A/ALPHA-E CHAIN PRECURSOR
8018	20015		0.56	1.0E-06	BE185330.1	EST_HUMAN	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
8334	21303		0.75	1.0E-06	AA912623.1	EST_HUMAN	q28c08.s1 Soares, NEL T, GBC S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8816	21584	35000	1.05	1.0E-06	A1347010.1	EST_HUMAN	q54602.x1 NCI_CGAP_Lyng8 Homo sapiens cDNA clone IMAGE:1926842 3'
8833	21800	35219	1.26	1.0E-06	A1287878.1	EST_HUMAN	q123106.x1 NCI_CGAP_Lyng8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element M1R repetitive element
9659	22816	36270	1.15	1.0E-06	N74635.1	EST_HUMAN	z55501.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:286472 3'
9734	22762	36217	0.55	1.0E-06	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
10041	22668	35434	3.97	1.0E-06	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
10041	22668	36435	3.97	1.0E-06	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
10085	23012	36486	4.9	1.0E-06	AA132611.1	EST_HUMAN	z07468.t1 Stragene colon (#637204) Homo sapiens cDNA clone IMAGE:687174 5'
10147	23073					EST_HUMAN	z044311.s1 Soares, total, fetus, NB2H.F8, 9w Homo sapiens cDNA clone IMAGE:785493 3' similar to
10854	23774		3.86	1.0E-06	AA448257.1	EST_HUMAN	bb-D26126 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
11650	24639		2.02	1.0E-06	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12672	15031	28040	3.14	1.0E-06	AW690941.1	EST_HUMAN	RC4-NT10094-120500-072-603 NT10094 Homo sapiens cDNA
12672	15031	28041	1.71	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
12672	15031	28041	1.71	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
380	13447	26374	1.95	9.0E-07	AF003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
380	13447	26375	1.95	9.0E-07	AF003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8750	17118	26375	0.59	9.0E-07	AL163290.2	NT	Homo sapiens chromosome 21 segment HS21C080
8808	21864		0.43	9.0E-07	AA448276.1	EST_HUMAN	z043101.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:782833 3'
11577	24515	38070	4.11	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4804	17821	30715	3.87	8.0E-07	AI288596.1	EST_HUMAN	ql8207.x1 Soares_NHNPu_S1 Homo sapiens cDNA clone IMAGE:1878878 3'
4804	17821	30716	3.87	8.0E-07	AI288596.1	EST_HUMAN	ql8207.x1 Soares_NHNPu_S1 Homo sapiens cDNA clone IMAGE:1878878 3'
5888	19073		8.55	8.0E-07	P21414	SWISSPROT	POLYPROTEIN CONTAINS; PROTEASE: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8335	21304		11.24	8.0E-07	AF195416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11843	24823		5.78	8.0E-07	T07723	EST_HUMAN	EST05690 Fetal brain, Stragene (Cell936206) Homo sapiens cDNA clone HFBN89
12183	25031		9.17	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5597	18693	31693	0.73	7.0E-07	6005700	NT	Homo sapiens A1P-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5597	18693	31694	0.73	7.0E-07	6005700	NT	Homo sapiens A1P-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1928	14852	27848	4.99	6.0E-07	AW855588.1	EST_HUMAN	CM3-CT0277-221059-024-e11 CT0277 Homo sapiens cDNA
2500	15503						Homo sapiens HLA class III region containing tarasin X (tarasin-X) gene, partial cds, cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes>
3986	17036		5.38	6.0E-07	AF019413.1	NT	HYPOPHYSICAL 24.1 KD PROTEIN IN LEF4P33 INTERGENIC REGION
9497	22461	35902	2.17	6.0E-07	BF001867.1	EST_HUMAN	789407.x1 NC1_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:075620 OT5620 4F5L.1
12442	25080		3.45	6.0E-07	AW903222.1	EST_HUMAN	CM4-NT0209-250300-121-112 NN1026 Homo sapiens cDNA
326	13417		0.99	5.0E-07	AI831863.1	EST_HUMAN	WH6410.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1080	14106		2.45	5.0E-07	AA390630.1	EST_HUMAN	EST83815 Suet cells Homo sapiens cDNA 5' end
3044	16101		0.86	5.0E-07	AI831863.1	EST_HUMAN	WH6410.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4976	17697	30584	1.16	5.0E-07	AF148774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6242	18315	32545	1.23	5.0E-07	U65067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
7266	20001	33300	1.68	5.0E-07	AI933981.1	EST_HUMAN	tg0805.x1 NC1_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107653 3' similar to contains Alu repetitive element; contains element A3R, repetitive element
7266	20001	33301	1.98	5.0E-07	AI933981.1	EST_HUMAN	tg0805.x1 NC1_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107653 3' similar to contains Alu repetitive element; contains element A3R, repetitive element
7571	20634	33892	15.74	5.0E-07	AW070885.1	EST_HUMAN	xs31a02.x1 NC1_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2566362 3' similar to gb:X16341
8618	21586	35002	0.87	5.0E-07	Q8WUQ1	SWISSPROT	CYTCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8635	21802		1.88	5.0E-07	P06563	SWISSPROT	ADAM-TS 1 (ADAMTS-1) (ADAM-TS1)
10732	23654	37147	5.39	5.0E-07	AI906587.1	EST_HUMAN	ADAM-TS 1 (ADAMTS-1) (ADAM-TS1)
11845	24728	38314	3.52	5.0E-07	P11087	SWISSPROT	SMANTIGEN (PROTEIN PRECURSOR
11806	24787		2.12	5.0E-07	AJ271755.1	NT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
12642	25780		4.14	5.0E-07	AW862537.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
							GIVC-CT0383-210400-204-512 CT0383 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4024	17062	29584	1.61	4.0E-07	AW009802.1	EST_HUMAN	w84105.x1 NCI CGAP Cx3 Homo sapiens cDNA clone IMAGE:2504697.3'
7384	20354		0.81	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7482	20448	33804	1.3	4.0E-07	Q82ZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HDS) (HISTONE DEACETYLASE MHDA1)
7482	20448	33805	1.3	4.0E-07	Q82ZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HDS) (HISTONE DEACETYLASE MHDA1)
8255	21224	34534	0.53	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8498	22371	35906	5.52	4.0E-07	AW419134.1	EST_HUMAN	x44911.x1 NCI CGAP Lx34.1 Homo sapiens cDNA clone IMAGE:2856548.3'
10486	23408	36904	0.46	4.0E-07	BE001975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651.5'
10486	23408	36905	0.46	4.0E-07	BE001975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651.5'
10688	23610	37105	0.47	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11284	24234	37760	2.6	4.0E-07	AJ1765528.1	EST_HUMAN	w81108.x1 NCI CGAP Kd12 Homo sapiens cDNA clone IMAGE:2398703.3'
11284	24234	37761	2.6	4.0E-07	AJ1765528.1	EST_HUMAN	w81108.x1 NCI CGAP Kd12 Homo sapiens cDNA clone IMAGE:2398703.3'
11555	24495		2.72	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
441	13515	28446	4.77	3.0E-07	U19719.1	NT	Human microtubulin-associated glycoprotein (MIFAP2) gene, putative promoter region and alternatively spliced untranslated exons
585	13653	26567	3.11	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1375	14409	27376	2.82	3.0E-07	M69149.1	NT	Human polymorphic microsatellite DNA
1630	14683		2.45	3.0E-07	M64857.1	NT	Human Igk subgroup I germline gene, exons 1 and 2, V-region 018 allele
2082	15080		1.01	3.0E-07	AA526783.1	EST_HUMAN	nt56509.st NCI CGAP OV2 Homo sapiens cDNA clone IMAGE:390825 similar to contains Alu repetitive element, contains L1.0 L1 repetitive element
2296	15308	28530	2.56	3.0E-07	M69149.1	NT	Human polymorphic microsatellite DNA
2477	15481	28505	8.03	3.0E-07	BE005077.1	EST_HUMAN	MFO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2477	15481	28506	8.03	3.0E-07	BE005077.1	EST_HUMAN	MFO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3047	16104	29018	0.8	3.0E-07	T84704.1	EST_HUMAN	YD072721 Sources fetal liver spleen TNF15 Homo sapiens cDNA clone IMAGE:11695.5'
3173	16228	29144	1.71	3.0E-07	P38739	SWISSPROT	HYPOPHYSICAL 63.8 KD PROTEIN IN GUT1-RIMT INTERGENIC REGION PRECURSOR
4708	17127		0.74	3.0E-07	P20740	SWISSPROT	OYOS1A1IN PRECURSOR (OYOMACROGLOBULIN)
4758	17778	30673	8.86	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLC0001.3'
4786	17813	30706	0.81	3.0E-07	AJ197238.1	EST_HUMAN	w66912.x1 Sources_NFL_T_GGC_S1 Homo sapiens cDNA clone IMAGE:2347667.3'
5103	18113	30995	2.02	3.0E-07	T57850.1	EST_HUMAN	yc14106.st Stragene lung (#637210) Homo sapiens cDNA clone IMAGE:30705.3' similar to similar to
5103	18113	30986	2.02	3.0E-07	T57850.1	EST_HUMAN	gbM62382 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5748	18943	32028	9.02	3.0E-07	O68607	SWISSPROT	yc14106.st Stragene lung (#637210) Homo sapiens cDNA clone IMAGE:30705.3' similar to similar to
6035	19165	32377	0.73	3.0E-07	O46290	SWISSPROT	gbM62382 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
							PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
							(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
							WNT-14 PROTEIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6881	19914		5.12	3.0E-07	AA816175.1	EST_HUMAN	cc04c10.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336890 3'
7752	20705	34074	3.26	3.0E-07	AW787168.1	EST_HUMAN	QV1-UM00396-2030300-115-g02 UM00396 Homo sapiens cDNA
7925	20868		1.09	3.0E-07	AI591065.1	EST_HUMAN	hw2811.x1 NCL CGAP_Ov65 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element NSR1; NSR1 repetitive element;
13083	26614		7.27	3.0E-07	AI152352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
31	13161	26051	4.19	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting isomeric RAP1 protein (RAP1) mRNA, complete cds
155	13258	25185	6.64	2.0E-07	L77568.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
155	13258	25186	6.64	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
183	13283	25209	152.51	2.0E-07	U38949.1	NT	Fugu ubipectus beta-cytoplasmic (vesicular) actin gene, complete cds
749	13810	26751	1.29	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
749	13810	26752	1.29	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
760	13820		0.87	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
942	13895	26947	3.12	2.0E-07	AA223290.1	EST_HUMAN	z08b07.s1 Striatagene NT2 neuronal precursor 937220 Homo sapiens cDNA clone IMAGE:650859 3' similar to gb.L11680 GLYCOPHORIN A PRECURSOR (HUMAN) contains Alu repetitive element;
943	13905	26948	7.18	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Striatagene lung (8937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element;
1167	14208	27162	1.16	2.0E-07	Q26768	SWISSPROT	I/6 AUTOANTIGEN
1604	14636	27613	2.35	2.0E-07	Q09701	SWISSPROT	HYPOHETICAL 72.5 KD PROTEIN C27.10 IN CHROMOSOME 1
3633	16676		0.86	2.0E-07	BF131397.1	EST_HUMAN	801818916F1 NIH IMG_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3700	16743	29656	17.94	2.0E-07	AF125348.1	NT	Homo sapiens cavedin 1 (CAV1) gene, exon 3 and partial cds
4196	17226	30115	1.42	2.0E-07	AI873563.1	EST_HUMAN	wk20H04.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2412918 3'
5417	18520	31397	1.71	2.0E-07	AW698056.1	EST_HUMAN	RC3.NN0065-260400-021-411 NN0068 Homo sapiens cDNA
6702	26666	33037	0.9	2.0E-07	AW446968.1	EST_HUMAN	UI-H-B13-aka-5-01-0-J1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734008 3'
6820	19874	33163	1.03	2.0E-07	AI208716.1	EST_HUMAN	qg56605.x1 Soares testis, NIH Homo sapiens cDNA clone IMAGE:1839177 3'
6832	19895	33178	0.81	2.0E-07	AA572953.1	EST_HUMAN	nm33a06.s1 NCL CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1081938 similar to contains Alu repetitive element;
8813	21780		4.23	2.0E-07	AW729390.1	EST_HUMAN	AT729390 HTC Homo sapiens cDNA clone HTCAE002 5'
9043	22009	35450	0.89	2.0E-07	AA035198.1	EST_HUMAN	z277509.s1 Soares_pregnant_uterus, NIH HU Homo sapiens cDNA clone IMAGE:471808 3'
10119	23045		1.8	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10030	23352	37052	6.11	2.0E-07	AW892507.1	EST_HUMAN	GM4.NN0003-280300-124-e08 NN0003 Homo sapiens cDNA COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF-2)
10855	23775	37272	0.92	2.0E-07	P00751	SWISSPROT	

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Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10855	23775	37273	0.92	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
12138	25503		2.86	2.0E-07	BE163717.1	EST_HUMAN	GLYCINE-RICH BETA GLYCOPROTEIN (GBG) (PBF2)
12224	25781		1.86	2.0E-07	A1732462.1	EST_HUMAN	zn88h1.x5 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR-02 THR repetitive element
1104	14148		1.46	1.0E-07	AL183282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2838	14558	27529	2.95	1.0E-07	P03256	SWISSPROT	GLYCOPROTEIN GPV
3757	14148		1.25	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4321	17350	30234	3.01	1.0E-07	AV178662.1	EST_HUMAN	AY178662 GLC Homo sapiens cDNA clone GLOFNFD4 5'
4321	17350	30235	3.01	1.0E-07	AV178662.1	EST_HUMAN	AY178662 GLC Homo sapiens cDNA clone GLOFNFD4 5'
6852	19709	32986	0.82	1.0E-07	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L12
7050	20072	33378	4.44	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Bri52 Homo sapiens cDNA clone IMAGE:2291339 5'
7050	20072	33379	4.44	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Bri52 Homo sapiens cDNA clone IMAGE:2291339 5'
7735	20690	34054	9.42	1.0E-07	NS5081.1	EST_HUMAN	Yv43d07.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:245484 3'
7910	20853	34240	0.69	1.0E-07	BF375909.1	EST_HUMAN	PMA-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7910	20853	34241	0.69	1.0E-07	BF375909.1	EST_HUMAN	PMA-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7940	20892	34272	1.27	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8558	21526	34944	2.28	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8558	21526	34945	2.28	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
9008	22271	35702	2.83	1.0E-07	AA603576.1	EST_HUMAN	ADAMTS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAMTS-8) (METH-2)
9625	22569	38018	0.96	1.0E-07	P57110	SWISSPROT	ADAMTS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAMTS-8) (METH-2)
9675	22902	38366	0.53	1.0E-07	BE327843.1	EST_HUMAN	h428h06.x1 NCI_CGAP_Met15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
10296	23221	38705	2.5	1.0E-07	BF674524.1	EST_HUMAN	h428h06.x1 NCI_CGAP_Met15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
10304	23229	38712	1.26	1.0E-07	AA388311.1	EST_HUMAN	692137714.F1 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:4274426 5'
10831	23752		2.53	1.0E-07	AL163282.2	NT	EST185054 Brain IV Homo sapiens cDNA
12500	25756	31517	4.03	1.0E-07	BE048770.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
12634	25320		1.69	1.0E-07	X64467.1	NT	DJ116331.1
12783	25423		1.89	1.0E-07	X51755.1	NT	H sapiens ALAD gene for porphobilinogen synthase
7498	20463	33823	0.84	9.0E-08	AI59362.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
							h657806.x1 Soares_NFL1_OBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9683	22636		0.54	6.0E-08	AA827075.1	EST_HUMAN	db560c5.61 NCI_CGAP_GG91 Homo sapiens cDNA clone IMAGE:1335388.3 similar to contains MER12.b3 MER12 repetitive element;
11744	24029	38208	1.91	5.0E-08	P11360	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
85	19201	26126	3.22	5.0E-08	AL163303.2	NT	ENDONUCLEASE]
2245	15259	28266	1.95	5.0E-08	AA493851.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
12165	25032		10.16	5.0E-08	P06691	SWISSPROT	element;
12382	25162	31814	1.63	5.0E-08	AW851878.1	EST_HUMAN	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
1775	14804	27789	1.07	4.0E-08	P25723	SWISSPROT	QV6-CT0225-131.089.034-412 CT0225 Homo sapiens cDNA
1775	14804	27789	1.07	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
3077	16134		0.95	4.0E-08	AI078417.1	EST_HUMAN	o2d5o2.x1 Scores: fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674458.3 similar to contains Alu repetitive element;
3834	16974	29808	0.76	4.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6545	19606	32608	0.91	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
9150	22116	35542	0.6	4.0E-08	O15390	SWISSPROT	TRANSMEMBRANE PROTEIN; SERINE 2
9494	22458	35808	1.32	4.0E-08	L42571.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
10093	22830		0.82	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10893	23615		0.65	4.0E-08	AI016342.1	EST_HUMAN	cd78d12.x1 Scores: total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622903.3
10752	23674	37171	3.67	4.0E-08	AI050027.1	EST_HUMAN	an2d10.x1 Geslar Wilms tumor Homo sapiens cDNA clone IMAGE:1680411.3 similar to contains Alu repetitive element; contains element MER22 repetitive element;
11411	24355	37859	1.51	4.0E-08	AA393827.1	EST_HUMAN	z7f6b08.r1 Scores: testis_NHT Homo sapiens cDNA clone IMAGE:728247.5 similar to TR:G505579
11411	24355	37859	1.51	4.0E-08	AA393827.1	EST_HUMAN	G505579 NA/CAL-K-EXCHANGER;
11411	24355	37860	1.51	4.0E-08	AA393827.1	EST_HUMAN	G505579 NA/CAL-K-EXCHANGER;
11426	24370	37907	3.11	4.0E-08	BF692483.1	EST_HUMAN	602248024F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4333300.5
11426	24370	37908	3.11	4.0E-08	BF692483.1	EST_HUMAN	602248024F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4333300.5
12190	25007		4.96	4.0E-08	W76159.1	EST_HUMAN	z6b5q03.r1 Scores: fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:3455596.5 similar to contains L1.11.1 repetitive element;
12830	25448		1.84	4.0E-08	AI343353.1	EST_HUMAN	ib95a11.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2082076.3 similar to contains MER18.b3
3439	16485	29404	0.94	3.0E-08	M83242.1	NT	MER18 MER18 repetitive element;
5692	18787	31956	3.06	3.0E-08	BE018348.1	EST_HUMAN	Macaca fascicularis epolipoprotein A-1 gene, complete cds
							bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570.5 similar to TR:Q92158 Q92158
							SYNTAXIN 17;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7168	18399	31245	4.23	3.0E-08	AI92737.1	EST_HUMAN	q76f11.y5 NCL_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:1844045 5'
7787	20740	34113	1.41	3.0E-08	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8025	20962		3.85	3.0E-08	AI436352.1	EST_HUMAN	h43h09.x1 Soares NSF F8_9w_OT_PA_P_31 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TF-O13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
10258	23183		0.57	3.0E-08	AF055066.1	NT	Homo sapiens MHC class 1 region
12157	25013		2.76	3.0E-08	R18420.1	EST_HUMAN	Y92D04.r1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element
207	13308		10.54	2.0E-08	AW302666.1	EST_HUMAN	xc9706.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2787139 3'
230	13330		8.83	2.0E-08	AA425589.1	EST_HUMAN	Alu repetitive element; contains element MER15 repetitive element ;
497	13569	26492	1.3	2.0E-08	AF198348.1	NT	zxc4807.r1 Soares, fetal, fetus, Nk2Hf8_0w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains repetitive element; contains element MER15 repetitive element ;
581	13727	26651	9.73	2.0E-08	AW886438.1	EST_HUMAN	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
581	13727	26652	9.73	2.0E-08	AW886438.1	EST_HUMAN	MR0-OT0080-240200-001-gp08 OT0080 Homo sapiens cDNA
592	14044		17	2.0E-08	BE260477.1	EST_HUMAN	MR0-OT0080-240200-001-gp08 OT0080 Homo sapiens cDNA
1346	14381	27350	1.93	2.0E-08	AL163247.2	NT	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138863 5'
1755	14784		1.87	2.0E-08	BE734871.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
1872	14897		3.57	2.0E-08	AW270271.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5'
2550	15552		1.7	2.0E-08	K00216.1	NT	xp4311.x1 NCL_CGAP_Pt111 Homo sapiens cDNA clone IMAGE:2743149 3'
3221	16276	26200	8.15	2.0E-08	O42280	SWISSPROT	Sheep Hic-rRNA-GUG
3221	16276	26201	8.15	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3873	16912		1.62	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161089-012-803 ST0197 Homo sapiens cDNA
4104	17138	30033	0.68	2.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4434	17481		1.2	2.0E-08	AA459040.1	EST_HUMAN	aa28c07.r1 NCL_CGAP_QCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1, L2 L1 repetitive element ;
4994	18009		2.97	2.0E-08	AW572881.1	EST_HUMAN	he7708.x2 NCL_CGAP_QML1 Homo sapiens cDNA clone IMAGE:2818327 3' similar to contains Alu repetitive element ;
5719	18813	31992	1.26	2.0E-08	AA813204.1	EST_HUMAN	al00411.s1 Soares Testis_NHT Homo sapiens cDNA clone 1377189 3'
5932	19018	33213	0.99	2.0E-08	AV088824.1	EST_HUMAN	xd32c04.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:266462 3' similar to contains MER18, L3
8337	21308	34721	1.86	2.0E-08	P10272	SWISSPROT	MER18 MER18 repetitive element ;
8447	21416	34629	1.47	2.0E-08	AA480121.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9440	22404		0.77	2.0E-08	AU139978.1	EST_HUMAN	ad02g06.a1 Scraligene total retina 937202 Homo sapiens cDNA clone IMAGE:396974 3'
							AU139978 PLACE1 Homo sapiens cDNA clone PLACE101719 5'



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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10886	23806	37310	0.8	2.0E-08	N78097.1	EST_HUMAN	y77202.1 Scores fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.53 LTR1 repetitive element
10886	23806	37311	0.8	2.0E-08	N78097.1	EST_HUMAN	y77202.1 Scores fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.53 LTR1 repetitive element
12472	25221	37311	1.88	2.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12882	25953		1.4	2.0E-08	11431678	NT	Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA
1510	15870	27513	1.42	1.0E-08	P31792	SWISSPROT	POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1760	14819	27804	2.12	1.0E-08	AF12546.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
2067	15084		2.49	1.0E-08	BE141959.1	EST_HUMAN	PM2-HT10130-150669-401-H12 HT10130 Homo sapiens cDNA
3206	16261	29181	1.19	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project-TCBA Homo sapiens cDNA clone TCBAP5232
3206	16261	29182	1.19	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project-TCBA Homo sapiens cDNA clone TCBAP5232
5680	18775	31947	4.5	1.0E-08	AJ010770.1	NT	Homo sapiens hypoxanthine phosphoribosyl transferase, exon 1-50
8046	20683	34380	0.98	1.0E-08	P19474	SWISSPROT	52 KD RO PROTEIN (SJOGEREN SYNDROME TYPE A ANTIGEN (SS-A)) (ROSS-A))
8069	21338	34749	0.47	1.0E-08	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
8406	21435	34852	0.56	1.0E-08	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
8406	21435	34853	0.56	1.0E-08	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
8892	21836	35280	1.89	1.0E-08	AJ015304.1	EST_HUMAN	(UBE2D3) genes, complete cds
9559	22521		0.46	1.0E-08	P09593	SWISSPROT	alpha3a5.51 Scores, testis tNFT Homo sapiens cDNA clone IMAGE:1618736 3'
9560	23522	35970	0.68	1.0E-08	BE072572.1	EST_HUMAN	S-ANTIGEN PROTEIN PRECURSOR
10925	23841	36728	0.81	1.0E-08	P79110	SWISSPROT	PM2-B10546-210100-404-402 B10546 Homo sapiens cDNA
10925	23841	37357	0.87	1.0E-08	P98053	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (GTP)
11644	24581	38149	3.4	1.0E-08	AF044083.1	NT	(TRICARBOXYLATE CARRIER PROTEIN)
12129	24698	38602	1.5	1.0E-08	P29315	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12129	24698	38603	1.5	1.0E-08	P29315	SWISSPROT	Homo sapiens major histocompatibility locus class III region
12569	25521		3.12	1.0E-08	X51755.1	NT	RIBONUCLEASE INHIBITOR
12640	25250		1.68	1.0E-08	X51755.1	NT	RIBONUCLEASE INHIBITOR
4271	17300	30170	4.15	9.0E-09	AL163279.2	NT	Human lambda-immunoglobulin constant region complex (germline)
4271	17300	30180	4.15	9.0E-09	AL163279.2	NT	Human lambda-immunoglobulin constant region complex (germline)
10422	23344		0.53	9.0E-09	197950.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
							y58a12.51 Scores fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:121918 3'

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6628	19686		1.59	8.0E-09	AJ270815.1	EST_HUMAN	q68c11.x1 NC1 CGAP_Gas4 Homo sapiens cDNA clone IMAGE:197894 3' similar to contains L1,13 L1 repetitive element;
7479	20448	33801	7.91	8.0E-09	A183500.1	EST_HUMAN	q42d07.x1 Scores: fetal heart Nhlh19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR.111 MSR1 repetitive element;
8333	21302	34719	3.04	8.0E-09	AW900159.1	EST_HUMAN	CMH-HNT1004-10300-273-400 NNT1004 Homo sapiens cDNA
8240	22305		2.64	8.0E-09	AJ93892.1	EST_HUMAN	q74d08.s1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
3021	16894		1.91	7.0E-09	D68942.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4034	17072		1.22	7.0E-09	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
8234	21203		0.56	7.0E-09	BF108755.1	EST_HUMAN	contains MER2b.b2 MER2b repetitive element;
8382	21351		0.91	7.0E-09	AA256200.1	EST_HUMAN	zr80c05.1 Scores: NHHWPU_S1 Homo sapiens cDNA clone IMAGE:881992 5' similar to contains L1,12 L1 repetitive element;
9815	22559	36008	3.06	7.0E-09	L09705.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10543	23465	36690	1.17	7.0E-09	BE254850.1	EST_HUMAN	60111173F1NH_MSC_18 Homo sapiens cDNA clone IMAGE:3351834 5'
10711	23633		0.59	7.0E-09	AA036626.1	EST_HUMAN	zr58d07.s1 Scores: fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121918 3'
11032	23968		3.65	7.0E-09	T87650.1	EST_HUMAN	yes8a12.s1 Scores: H1434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0514 5'
2162	15178		0.98	8.0E-09	AL04039.1	EST_HUMAN	DKFZp434C0514.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0514 5'
4059	17095	25690	0.96	8.0E-09	AA557940.1	EST_HUMAN	n17a11.s1 NC1 CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1,12 L1 repetitive element;
5017	18031	30517	5.44	8.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-401-H05 HT0527 Homo sapiens cDNA
5454	18566	31467	9.55	8.0E-09	AW195784.1	EST_HUMAN	xn85h03.x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8622	21888	35315	0.88	8.0E-09	BE161653.1	EST_HUMAN	MR3-HT0446-260300-201-H12 HT0446 Homo sapiens cDNA
9531	22494	35942	2.12	8.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10639	23681		4.42	8.0E-09	AF200323.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
1413	14448	27418	4.43	5.0E-09	BE149284.1	EST_HUMAN	KC2-HT0252-120200-014-H10 HT0252 Homo sapiens cDNA
1970	14895	27894	1.02	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
8550	19811	32872	2.31	5.0E-09	AA3393454.1	EST_HUMAN	EST188748 Fetal lung II Homo sapiens cDNA 5' end
7025	18957	31277	0.56	5.0E-09	U6659.1	NT	Human geminin T-cell receptor beta chain Dopamine-beta-hydroxylase-like TRY1, TRY2, TRY3, TCRBV2/5'P, TCRBV2/5'IA2N1T, TCRBV5/5'IA1T, TCRBV5/5'IA1T, TCRBV13S3, TCRBV6/5'P, TCRBV7/5'3A2T, TCRBV13S2A1T, TCRBV6S2A2P1T, TCRBV7S2A1N4T, TCRBV13S3N13S3>

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8622	21888	35326	0.5	3.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
10455	23377	36870	2.53	5.0E-09	AJ796687.1	EST_HUMAN	PM2-UMD033-240300-005-c09 UMD033 Homo sapiens cDNA
522	13593		1.81	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
966	14018		2.79	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1465	14486	27472	2.79	4.0E-09	9558718	NT	Homo sapiens hypothetical protein AF038169) mRNA
2038	15057	28078	1.53	4.0E-09	AF17525.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2038	15057	28078	1.63	4.0E-09	AF17525.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2436	15443	28461	2.87	4.0E-09	AA350878.1	EST_HUMAN	EST198358 Infant brain Homo sapiens cDNA 5' end similar to heat shock protein, 90 kDa
8170	21149	34556	0.66	4.0E-09	AA485747.1	EST_HUMAN	z040406.1) Soares. NIHMPU_S1 Homo sapiens cDNA clone IMAGE:788288 5'
8887	21834	35235	0.68	4.0E-09	T64942.1	EST_HUMAN	x11607.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:96804 3'
2359	15367	28389	4.28	3.0E-09	BE222239.1	EST_HUMAN	h039409.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2560	15561	28579	1.39	3.0E-09	BE222239.1	EST_HUMAN	h039409.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2569	15566	28674	1.03	3.0E-09	P23249	SWISSPROT	MER18 repetitive element; PROTEIN MOV-10
3340	16391	29312	1.15	3.0E-09	BE222239.1	EST_HUMAN	h039409.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
3388	16437		0.79	3.0E-09	AA442272.1	EST_HUMAN	MER18 repetitive element; z05404.1) Soares. testis_NHT Homo sapiens cDNA clone IMAGE:787422 5'
4124	17157		0.69	3.0E-09	X16674.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4457	17483	30371	3.77	3.0E-09	AF17525.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4540	17683	30450	3.44	3.0E-09	Q913R5	SWISSPROT	288.1 KDA PROTEIN C21ORF5 (KIA06933)
5225	18233		0.99	3.0E-09	D96842.1	NT	Homo sapiens DNA for 3-ketoadipyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
8232	21201	34607	1.08	3.0E-09	BE465780.1	EST_HUMAN	h080a02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TFR:O55091
10069	23531	37026	1.84	3.0E-09	AL163247.2	NT	O55091 IMPACT PROTEIN.1
11361	24310	37656	3.06	3.0E-09	BF106943.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
11361	24310	37637	3.06	3.0E-09	BF106943.1	EST_HUMAN	777208.x1 Soares. NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
813	13871		10.64	2.0E-09	X16674.1	NT	777208.x1 Soares. NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1263	14298	27261	5.84	2.0E-09	AL163284.2	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1667	14669	28366	9.53	2.0E-09	AL118573.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
2334	15346	28366	2.58	2.0E-09	Q913R5	SWISSPROT	DKFZ761B1710.1 1761 (synonym: hamy2) Homo sapiens cDNA clone DKFZ761B1710 5'
3958	16968	29913	3.67	2.0E-09	O60241	SWISSPROT	286.1 KDA PROTEIN C21ORF5 (KIA06933)
4039	17077	29977	1.65	2.0E-09	AJ263470.1	EST_HUMAN	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
							x107d09.x1 Soares. NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1855793 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5198	18307	31081	0.88	2.0E-09	M23161.1	NT	Human transposon-like element mRNA
5808	18898	32081	0.69	2.0E-09	A100482.1	EST_HUMAN	cd47b0.9 x1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1619897 3'
6273	18348		0.85	2.0E-09	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C049
6947	20171		0.8	2.0E-09	AA357407.1	EST_HUMAN	EST168142 Kidney IX Homo sapiens cDNA 5' and similar to EST containing L1 repeat
7694	20642	34006	7.6	2.0E-09	AA461430.1	EST_HUMAN	z63908.r1 Soares, total, fetus, Nb2-IF8_gy Homo sapiens cDNA clone IMAGE:786187 5' similar to contains Alu repetitive element;
7768	20719	34032	0.63	2.0E-09	W28834.1	EST_HUMAN	52411 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8126	21063	34461	0.82	2.0E-09	AW602126.1	EST_HUMAN	MR1-CT0352-240200-105-006 CT0352 Homo sapiens cDNA
9062	22028	35452	2.25	2.0E-09	AJ271735.1	NT	Homo sapiens Xq1 pseudautosomal region, segment 1/2
12705	13871		22.38	2.0E-09	X16674.1	NT	H sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
12772	25975		1.67	2.0E-09	AA226070.1	EST_HUMAN	nc11602.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;
12778	25829		1.47	2.0E-09	AW301637.1	EST_HUMAN	x59602.x1 NCI_CGAP_Xk611 Homo sapiens cDNA clone IMAGE:2768234 3'
12813	25492		1.98	2.0E-09	U82998.1	NT	Homo sapiens atox gene, alternatively spliced products, complete cds
1111	14155	27105	1.1	1.0E-09	6031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1111	14155	27106	1.1	1.0E-09	6031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1638	14670		0.91	1.0E-09	AJ28041.1	NT	Homo sapiens 969 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2510	15513		1.16	1.0E-09	AJ356988.1	EST_HUMAN	q96441.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2018812 3' similar to contains MER12.12 MER12 repetitive element;
2900	15959	28878	1.83	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
2937	15955	28915	4.07	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2937	15955	28916	4.07	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3051	16108	29022	0.89	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
4836	17853		5.63	1.0E-09	AA719287.1	EST_HUMAN	z0105802.F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
5162	18171	31050	0.84	1.0E-09	T60216.1	EST_HUMAN	z035603.b1 Soares, pineal, gland_X34PFG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
5581	18677	31640	0.82	1.0E-09	AL163283.2	NT	yc22c09.r1 Svalgsigens lung (#937210) Homo sapiens cDNA clone IMAGE:81424 5' similar to contains Alu repetitive element; contains MER28 repetitive element;
5930	19016	32211	1.35	1.0E-09	U07000.1	NT	Homo sapiens chromosome 21 segment HS21C083
6267	19340	32572	3.11	1.0E-09	P26994	SW/ISSPROT	Human breakpoint cluster region (BCR) gene, complete cds
8113	21050	34448	0.63	1.0E-09	AV728645.1	EST_HUMAN	CIRCUMFOROZOTE PROTEIN PRECURSOR (CS)
8733	21701	35127	0.87	1.0E-09	AJ688474.1	EST_HUMAN	AV728645 HTC Homo sapiens cDNA clone HITCBIG07 5'
							x439045.x1 Soares, NFL, I, GBC, S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains MER25.11 MER25 repetitive element;

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10677	23599		2.87	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12081	24863		1.93	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12818	25916	31425	2.01	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12781	25416		1.6	1.0E-09	T83175.1	EST_HUMAN	ye24e05.11 Strategic lung (#837210) Homo sapiens cDNA clone IMAGE:118698 5'
1312	14348	27314	2.49	9.0E-10	AW867740.1	EST_HUMAN	MIR-SN0040-050500-202-407 SN0040 Homo sapiens cDNA
2845	15905	28930	6.64	9.0E-10	AI870071.1	EST_HUMAN	w678i03.x1 Soares, Diacografe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW.RL29_HUMAN P47614 80S RIBOSOMAL PROTEIN L29 contains element PTR3 repetitive element 1; f44806.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to TR000372 O00372 PUTATIVE P150 ;
7008	20134	33449	4.22	9.0E-10	AI452982.1	EST_HUMAN	Homo sapiens MC4A (MC4A) and DNA-PKcs (PRKDC) genes, partial cds
1468	13281	28180	12.13	9.0E-10	U63680.2	NT	Homo sapiens cDNA
3353	18404	29325	0.76	8.0E-10	BE080748.1	EST_HUMAN	QV17-BT0631-160200-071-101 BT0631 Homo sapiens cDNA
4229	17258	30142	3.69	8.0E-10	AA376832.1	EST_HUMAN	EST88964 Small intestine 1 Homo sapiens cDNA 5' and
10324	23248		2.46	8.0E-10	U93036.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
702	13764	26598	32.88	7.0E-10	7708225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
702	13764	26598	32.88	7.0E-10	7708225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1626	14859	27596	2.48	7.0E-10	Q13342	SW/ISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2556	15697		21.64	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3104	16161	290721	2.89	7.0E-10	X00656.1	NT	H sapiens DHFR gene, exon 3
6309	18880	32619	3.72	7.0E-10	AA345220.1	EST_HUMAN	EST51247 Gall bladder 11 Homo sapiens cDNA 5' and
7647	20507	33973	1.2	7.0E-10	BF352883.1	EST_HUMAN	IL3-IT0619-110700-209-D12 HT0610 Homo sapiens cDNA
7918	20361		1.46	7.0E-10	P35034	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8308	21277	34688	1.29	7.0E-10	AF028701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
8308	21277	34689	1.29	7.0E-10	AF028701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
10673	23595	37092	0.68	7.0E-10	L08895.1	NT	Homo sapiens MAD5/MEF2-family transcription factor (MEF2C) mRNA, complete cds
914	13865	26922	2.67	6.0E-10	AJ400877.1	NT	Homo sapiens ASC13 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene and C11orf17 gene
2985	15682	28700	1.37	6.0E-10	AI424405.1	EST_HUMAN	RC3-OT0254-031099-012-g12 CT0254 Homo sapiens cDNA
4768	17785		2.72	6.0E-10	AW853718.1	EST_HUMAN	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
9135	22101	35527	0.89	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD68E)
9135	22101	35528	0.89	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
9992	22919	33396	0.43	6.0E-10	P98073	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD68E) ENTEROPYPTIDASE PRECURSOR (ENTEROKINASE)

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12221	25098		1.84	3.0E-10	AW971922.1	EST_HUMAN	EST7384012 IMAGE: rhesus, MAGL Homo sapiens cDNA
761	13821		5.01	5.0E-10	AL046804.1	EST_HUMAN	DKFZ434N219_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZ434N219 5'
3489	16595	29460	1.53	5.0E-10	Q01033	SWISSPROT	HYPOPHYSICAL GENE 48 PROTEIN
5026	18240	30923	1.1	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
7544	25057	35303	1.74	5.0E-10	BF105159.1	EST_HUMAN	601322184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
9894	22847	35303	1.95	5.0E-10	P34678	SWISSPROT	HYPOPHYSICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
9894	22847	35304	1.95	5.0E-10	P34678	SWISSPROT	HYPOPHYSICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
111	13222		1.27	4.0E-10	A1221083.1	EST_HUMAN	q009f09.x1 Soares, placenta, BioWeeks, 2NbHP869W Homo sapiens cDNA clone IMAGE:1758049 3'
583	13651	25665	0.75	4.0E-10	AA515260.1	EST_HUMAN	similar to contains LTRb2 LTR8 repetitive element;
2012	15033	28043	1.4	4.0E-10	AW594709.1	EST_HUMAN	h954601.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:924648 3'
2580	15581	28600	5.49	4.0E-10	AL163303.2	NT	repetitive element;
7382	20382	33703	17.71	4.0E-10	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C103
10955	23477	36971	0.83	4.0E-10	AW28243.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
10912	23733	37235	0.87	4.0E-10	AL287342.1	EST_HUMAN	U1-HB2-ahh-a-07-JUL1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727081 3'
10933	23853	37368	0.45	4.0E-10	BE165208.1	EST_HUMAN	eq68h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2095653
10933	23853	37369	0.45	4.0E-10	BE165208.1	EST_HUMAN	PM1-H10521-120200-001-168 HT0621 Homo sapiens cDNA
916	13970	28924	1.8	3.0E-10	N56113.1	EST_HUMAN	h93206.s1 Soares melanocyte 2Nb-HM Homo sapiens cDNA clone IMAGE:272993 3' similar to contains LTRb1 LTR1 repetitive element;
1353	14388		4.8	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
4566	17580	30480	1.04	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4860	17580	30481	1.04	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5530	18628	31564	1.06	3.0E-10	N50109.1	EST_HUMAN	h21108.s1 Soares, multiple sclerosis, 2NbHMSIP Homo sapiens cDNA clone IMAGE:282782 3'
6327	19397	32639	4.03	3.0E-10	P20590	SWISSPROT	RHOMBOD PROTEIN (VEINLET PROTEIN)
6486	19551	32801	3.08	3.0E-10	BE302970.1	EST_HUMAN	b676d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806319 5'
8036	20973	34367	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CSF8GD08 5'
8036	20973	34368	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CSF8GD08 5'
9082	22048	35471	1.04	3.0E-10	H87208.1	EST_HUMAN	x674b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER2B repetitive element;
9404	22369	35803	1.8	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9404	22369	35804	1.8	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9696	22649		0.73	3.0E-10	AF020303.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10828	23749		2.05	3.0E-10	T65891.1	EST_HUMAN	yc11tr12.1i Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80388 5'
10857	23877		1.76	3.0E-10	AA759284.1	EST_HUMAN	nc236g03.x1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289908 3'
12865	25488	31728	1.95	3.0E-10	BE179517.1	EST_HUMAN	IL3-IT0618-110500-138-E07 HT0618 Homo sapiens cDNA
37	26038	26038	1.55	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
37	13157	26039	1.55	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1913	14937		1.88	2.0E-10	U90017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p-4) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
2999	16057		0.68	2.0E-10	BF675047.1	EST_HUMAN	602136840F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5901	18988		3.12	2.0E-10	Q28640	SWISSPROT	(HPRC)
6379	19447	32688	1.55	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7803	20586	33926	6.24	2.0E-10	BE791082.1	EST_HUMAN	60158020F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
8347	21316	34730	0.54	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE: REVERSE TRANSCRIPTASE: RIBONUCLEASE H]
8347	21316	34731	0.54	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE: REVERSE TRANSCRIPTASE: RIBONUCLEASE H]
9657	22690		0.85	2.0E-10	BF434565.1	EST_HUMAN	7678d08.x1 NCI CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3842203 3' similar to contains L1.13 L1 repetitive element;
1509	14542		2.94	1.0E-10	AW567767.1	EST_HUMAN	MRO-SN0038-290300-001-101 SN0038 Homo sapiens cDNA
1611	14643	27619	3.27	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXA11 3'
2586	15887		1.92	1.0E-10	AW852001.1	EST_HUMAN	QVQ-CT0225-191189-058-e08 CT0225 Homo sapiens cDNA
3511	16557	29431	0.64	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161199-013-410 TT0003 Homo sapiens cDNA
3550	16596		0.81	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317.1 434 (synonym: Ites3) Homo sapiens cDNA clone DKFZp434N1317 5'
3550	16596		0.81	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317.1 434 (synonym: Ites3) Homo sapiens cDNA clone DKFZp434N1317 5'
3550	16596		0.94	1.0E-10	AL041685.1	EST_HUMAN	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4043	17081		6.46	1.0E-10	AF213884.1	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adenoleukodystrophy protein >
4154	17185	30072	5.55	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adenoleukodystrophy protein >
4154	17185	30073	5.55	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adenoleukodystrophy protein >
4160	17191	30080	2.48	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4199	17230		2.93	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5212	18221		0.92	1.0E-10	A179745.1	EST_HUMAN	w82004.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347813 3' similar to contains MER31.1t MER31 repetitive element;
6975	19628		0.91	1.0E-10	AA631233.1	EST_HUMAN	ng81ta05.s1 NCI CGAP_C68 Homo sapiens cDNA clone IMAGE:1158704 3'
6991	20214		0.49	1.0E-10	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7716	20673		0.56	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7947	20888		0.63	1.0E-10	AU126594.1	EST_HUMAN	AU126594 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8592	21550		1.11	1.0E-10	AW403600.1	EST_HUMAN	fB_SAX Fetal brain library Homo sapiens cDNA
9002	21968		1.1	1.0E-10	AI26340.1	EST_HUMAN	qnm4a10.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1860874 3' similar to contains L1.11 L1 repetitive element;
10562	23484		3.95	1.0E-10	AA081868.1	EST_HUMAN	zn25g06.11 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:546314 5'
11259	24211		3.25	1.0E-10	A1038280.1	EST_HUMAN	oy68h03.x1 Soares, fetal_liver_spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:1872861 3'
12166	18354		2.46	1.0E-10	X87344.1	NT	H sapiens DMA, DMB, HLA-Z1, PIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
281	13357	28282	0.98	9.0E-11	BE145600.1	EST_HUMAN	IL2-H10203-291099-016-c08 HT0203 Homo sapiens cDNA
2114	15131	28151	6.21	9.0E-11	AL134395.1	EST_HUMAN	DKFZp5647D225_11 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp5647D225 5'
2114	15131	28152	6.21	9.0E-11	AL134395.1	EST_HUMAN	DKFZp5647D225_11 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp5647D225 5'
3394	16443	29370	2.6	9.0E-11	AL134395.1	EST_HUMAN	DKFZp5647D225_11 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp5647D225 5'
3394	16443	29371	2.6	9.0E-11	AL134395.1	EST_HUMAN	DKFZp5647D225_11 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp5647D225 5'
4528	17552	30440	0.72	9.0E-11	AA776986.1	EST_HUMAN	ae78101.x1 Stratagene scilicet brain S11 Homo sapiens cDNA clone IMAGE:970287 3'
5654	18750		3.89	9.0E-11	BE079780.1	EST_HUMAN	RC8-BT0627-140200-Q11-E08 BT0627 Homo sapiens cDNA
10514	23436	36934	1.22	9.0E-11	AA324960.1	EST_HUMAN	EST17872 Cerebellum II Homo sapiens cDNA 5' end
10514	23436	36935	1.22	9.0E-11	AA324960.1	EST_HUMAN	EST17872 Cerebellum II Homo sapiens cDNA 5' end
12546	23266	31809	4.59	9.0E-11	C16635.1	EST_HUMAN	G16635 Clontech human cora polyA+ mRNA (46572) Homo sapiens cDNA clone GEN-506608 5'
3133	16190		8.85	9.0E-11	HI19871.1	EST_HUMAN	yn5311.1.s1 Soares adult brain N254H5537 Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
4073	17109	30003	4.35	9.0E-11	N23712.1	EST_HUMAN	yy46ed06.s1 Weizmann Officery Epithelium Homo sapiens cDNA clone IMAGE:255288 3'
5890	18978	32170	0.65	9.0E-11	AW674316.1	EST_HUMAN	ba66q04.x1 NHL MGCC_10 Homo sapiens cDNA clone IMAGE:2800982 3'
6829	19893		0.65	9.0E-11	AW168158.1	EST_HUMAN	x1AB11.x1 NCI CGAP_Bn150 Homo sapiens cDNA clone IMAGE:2821061 3' similar to contains MER10.1t MER10 repetitive element;
1442	14475	27452	1.87	7.0E-11	AA330542.1	EST_HUMAN	EST34392 Embryo, 8 week 1 Homo sapiens cDNA 5' end



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3885	16925	28834	1.11	7.0E-11	AJ27546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8843	21810	35228	2.79	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10590	23512		1.19	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
412	13465	28421	6.97	6.0E-11	M55270.1	NT	Human matrix Glp protein (MGP) gene, complete cds
412	13465	28422	6.97	6.0E-11	M55270.1	NT	Human matrix Glp protein (MGP) gene, complete cds
6894	16936	33232	0.88	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from flamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
7957	20988	34231	3.22	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8707	21675	35100	7.37	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCCSC08.5'
9668	22621	35072	0.42	6.0E-11	BE063509.1	EST_HUMAN	CM6-BT0281-031169-087-403 BT0281 Homo sapiens cDNA
12	13132	26030	0.75	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS2TC083
3377	13132	26030	1.31	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS2TC083
4266	17285	30187	1.51	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
6655	18722	32867	1.91	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS2TC013
7774	20727	34069	11.91	5.0E-11	11416799	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
1401	14434		1.68	4.0E-11	AA436042.1	EST_HUMAN	z01612.1 Scores, testis, testis_NHT Homo sapiens cDNA clone IMAGE:730559.5'
2802	15784	28812	7.83	4.0E-11	BE886900.1	EST_HUMAN	601607531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295.5'
2981	16039	28962	0.92	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS2TC047
4849	17670	30557	1.24	4.0E-11	D44686.1	EST_HUMAN	HUMSUPY068 Human brain cDNA Homo sapiens cDNA clone 009
5621	19679	32857	3.27	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
7197	20221	33552	0.54	4.0E-11	AA442630.1	EST_HUMAN	z6810.1 Scores, testis_NHT Homo sapiens cDNA clone IMAGE:787963.5' similar to TR.G1055250
7890	20561		3.97	4.0E-11	AF224699.1	NT	G1055250 PHEROMONE RECEPTOR VN4. ;
9750	22891		1.88	4.0E-11	BE149426.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10020	22847	36415	0.86	4.0E-11	AI609753.1	EST_HUMAN	RC1-H10256-210100-013-068 HT0256 Homo sapiens cDNA
12736	26388	31762	1.56	4.0E-11	11545732	NT	CE003985 ;
1488	14521	27484	2.55	3.0E-11	6676077	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
4305	17334		1.37	3.0E-11	AA309248.1	EST_HUMAN	Mus musculus expressed in non-mesodermal cells 2, protein (NM23B) (Nm2), mRNA
961	14014	26967	1.48	2.0E-11	AI150502.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
							q36c04.x1 Scores, testis_NHT Homo sapiens cDNA clone IMAGE:1752102.3' similar to contains MER10.8
							1/NER10 repetitive element;



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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12354	25148	31854	2.14	2.0E-11	BF377850.1	EST_HUMAN	GM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12817	25313		1.49	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12754	25399		1.68	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
13070	25604		3.68	2.0E-11	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
677	13740	26697	0.83	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
784	13844	26798	1.89	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1221	14259	27216	4.66	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1498	14531		2.95	1.0E-11	AF119814.1	NT	Homo sapiens PRQ3078 mRNA, complete cds
2053	15072	28091	1.41	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2108	15155	28168	3.18	1.0E-11	AF000573.1	NT	Homo sapiens homonitilicase 1,2-dioxygenase gene, complete cds
2170	15186	28207	1.15	1.0E-11	AA309318.1	EST_HUMAN	EST180186 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end similar to EST containing Alu repeat
3510	16556	29430	0.8	1.0E-11	BE004315.1	EST_HUMAN	GM2-BN0105-170300-282-412 BN0105 Homo sapiens cDNA
4860	17975	30896	1.01	1.0E-11	AI168625.1	EST_HUMAN	ox6506.p1 Soares, NIHMP1, S1 Homo sapiens cDNA clone IMAGE:1861243 3'
5405	18508	31385	14.43	1.0E-11	AL183247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5931	19017	32212	0.77	1.0E-11	BF222646.1	EST_HUMAN	7p57d01.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3
8112	21049		0.51	1.0E-11	AB042297.1	NT	MER10 repetitive element
8543	21511	34928	3.36	1.0E-11	4895548	NT	Homo sapiens PDS gene for 6-pyruvyltetrahydropterin synthase, complete cds
8828	21894	35322	4.18	1.0E-11	R13174.1	EST_HUMAN	yf73d08.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28166 5'
9403	22368	35801	1.18	1.0E-11	BF365119.1	EST_HUMAN	QVA-NT1149-250900-423-403 NT1149 Homo sapiens cDNA
9403	22368	35902	1.18	1.0E-11	BF365119.1	EST_HUMAN	QVA-NT1149-250900-423-403 NT1149 Homo sapiens cDNA
11619	24557	35120	1.48	1.0E-11	BF690078.1	EST_HUMAN	602154807F1 NIH MSC_83 Homo sapiens cDNA clone IMAGE:4285977 5'
2963	18021	28946	0.82	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10157	23082	36558	1.02	9.0E-12	AL163500.2	NT	Homo sapiens chromosome 21 segment HS21C100
10157	23082	36558	1.02	9.0E-12	AL163500.2	NT	Homo sapiens chromosome 21 segment HS21C100
12075	24947	38542	2.85	9.0E-12	AL046639.1	EST_HUMAN	DKFZp6600417.1 586 (synonym: hule1) Homo sapiens cDNA clone DKFZp6600417 5'
9893	22646		0.92	8.0E-12	BE074720.1	EST_HUMAN	IL5-B1 0578-130300-036-G12 BT0578 Homo sapiens cDNA
12407	25180		3.22	8.0E-12	AJ271736.1	NT	Homo sapiens Xa pseudotubercular region, segment 22
4590	17711	36065	1.48	7.0E-12	Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM84)
11617	24643	38220	7.41	7.0E-12	AA704735.1	EST_HUMAN	423g01.x1 Soares fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
3558	16604		0.95	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAVFO6 5'
							n288f1.x1 NCI CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu
4375	17403	30283	9.28	6.0E-12	AA732516.1	EST_HUMAN	repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6528	19591	32851	0.65	6.0E-12	AF029593.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
8247	22312	35738	0.98	6.0E-12	AF003249.1	NT	Macaca saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9820	22878		1.66	6.0E-12	AA847898.1	EST_HUMAN	cd1011.1 s1 NCL CGAP GC51 Homo sapiens cDNA clone IMAGE:1387588 similar to contains MER28.12
1044	14090	27043	3.57	5.0E-12	T06573.1	EST_HUMAN	MER28 repetitive element;
3401	18450	26378	1.17	5.0E-12	BE047719.1	EST_HUMAN	cd10462 Fetal brain, Stratiogene (cd1063620) Homo sapiens cDNA clone HFB01V33
3740	18782	29894	6.8	5.0E-12	AJ271736.1	NT	tx24005.v1 NCL CGAP_Bri52 Homo sapiens cDNA clone IMAGE:2291217 5'
6137	19214	32441	4.89	5.0E-12	AL16378.2	NT	Homo sapiens Xq pseudobacterial region; segment 2/2
6137	19214	32442	4.89	5.0E-12	AL16378.2	NT	Homo sapiens chromosome 21 segment HS21C078
6639	19697	32973	9.52	5.0E-12	AW674760.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
7232	19977	33274	1	5.0E-12	AL040739.1	EST_HUMAN	EST38850 IMAGE resequencing; MAGN Homo sapiens cDNA
7242	19977	33274	1.03	5.0E-12	AL040739.1	EST_HUMAN	DKFZ434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZ434B1615 3'
8571	21639	34990	1.14	5.0E-12	AA033745.1	EST_HUMAN	DKFZ434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZ434B1615 3'
9015	21881		0.7	5.0E-12	AW987037.1	EST_HUMAN	cd10112.s1 Soares fetal heart Nbt-H19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.9 L1 repetitive element;
8346	22311		0.54	5.0E-12	AL079581.1	EST_HUMAN	RC1-OT10086-220300-OT1-1007 OT10086 Homo sapiens cDNA
8464	22428	35807	2.78	5.0E-12	AJ271735.1	NT	DKFZ434J0426_L1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZ434J0426 5'
9778	22719	38173	1.38	5.0E-12	P34982	SWISSPROT	Homo sapiens Xq pseudobacterial region; segment 1/2
10538	23680		4.14	5.0E-12	AL163303.2	NT	OLFACTORY RECEPTOR 102 (OLFACTORY RECEPTOR-LIKE PROTEIN HGM07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10729	23851	37144	0.81	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C103
244	13342	26287	4.17	4.0E-12	AA700326.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
245	13342	26287	5.51	4.0E-12	AA700326.1	EST_HUMAN	2f74g11.s1 Soares fetal liver spleen INFLS_S1 Homo sapiens cDNA clone IMAGE:460678 3'
4650	17671	30658	0.74	4.0E-12	AI689984.1	EST_HUMAN	2f74g11.s1 Soares fetal liver spleen INFLS_S1 Homo sapiens cDNA clone IMAGE:460678 3'
7981	20825		0.72	4.0E-12	BF445140.1	EST_HUMAN	tx28005.s1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR.Q13539 Q13539 MARINER TRANSPOSASE.;
8685	21653		2.82	4.0E-12	AF109097.1	NT	na21603.s1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3368077 3' similar to contains MER7.02
9035	22001	35422	0.76	4.0E-12	AB042815.1	NT	MER7 repetitive element;
11419	24363	37898	3.26	4.0E-12	AJ226043.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
12668	25538		2.82	4.0E-12	U78027.1	NT	Bos taurus Mch2 mRNA for mitochondrial carrier homolog 2, complete cds
							Homo sapiens 959 kb contig between ANK1 and CBR1 on chromosome 21q22, segment 3/3
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
618	13683	26600	3.06	3.0E-12	AW341083.1	EST_HUMAN	h13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2969377 3' similar to TR.O14517
618	13683	26601	3.06	3.0E-12	AW341083.1	EST_HUMAN	O14617 SMRP.; h13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2969377 3' similar to TR.O14517
5211	18220	31098	0.73	3.0E-12	AF163268.2	NT	O14617 SMRP.; Homo sapiens chromosome 21 segment HS21C068
5527	18626	31562	0.96	3.0E-12	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
7659	20519		0.54	3.0E-12	A044297.1	NT	Homo sapiens PFS gene for G-pyruvylate hydrolysis synthase, complete cds
8030	20967		0.55	3.0E-12	AW854328.1	EST_HUMAN	RC3-CT0285-031099-011-h02 CT0285 Homo sapiens cDNA
8718	21686	35114	0.49	3.0E-12	OQ35453	SWISSPROT	SERINE PROTEASE HEPHSIN
9462	22426	35864	0.54	3.0E-12	OQ35453	SWISSPROT	SERINE PROTEASE HEPHSIN
11016	23681	37507	2.71	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
11016	23681	37508	2.71	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1681	14683	27658	2.41	2.0E-12	AW802131.1	EST_HUMAN	IL5-UM0071-120400-065-ab5 UM0071 Homo sapiens cDNA
3480	16526	29451	0.85	2.0E-12	6764465	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4141	17172	30060	1.09	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4141	17172	30061	1.09	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4451	17477		1.87	2.0E-12	BE063509.1	EST_HUMAN	GMD-BT0281-031199-087-ab3 BT0281 Homo sapiens cDNA
5321	18427	31177	0.71	2.0E-12	P11969	SWISSPROT	RETROVIRUS RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
6622	19680		1.83	2.0E-12	AW971857.1	EST_HUMAN	EST383946 MAGE sequences, MAGE, Homo sapiens cDNA
7351	20351	33702	3.22	2.0E-12	T08169.1	EST_HUMAN	EST08060 Infant Brain, Berto Soares Homo sapiens cDNA clone HIBBA13 5' end
7597	20530	33989	1.18	2.0E-12	BE173036.1	EST_HUMAN	MR0-HT0559-200400-015-e08 HT0559 Homo sapiens cDNA
7778	20731		0.57	2.0E-12	AW842798.1	EST_HUMAN	MR2-CN0037-210200-101-502 CN0037 Homo sapiens cDNA
7922	20865	34253	2.1	2.0E-12	11422229	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
9077	22043	35468	0.43	2.0E-12	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAC-T1)
8663	22820		1.65	2.0E-12	AF196864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
10345	23269		14.41	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-165020-113-g01 HT0487 Homo sapiens cDNA
10881	23801	37304	0.8	2.0E-12	A334130.1	EST_HUMAN	qp0702.x1 Soares_NHMP2u_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR-Q13538
12308	25116		3.11	2.0E-12	AL103283.2	NT	Q13538 ORF2: FUNCTION UNKNOWN.
12511	25245		1.69	2.0E-12	11418248	NT	Homo sapiens chromosome 21 segment HS21C083
							Homo sapiens sulfotransferase-related protein (SULTX3), mRNA

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
123	13231	28159	2.83	1.0E-12	AW827874.1	EST_HUMAN	h90a03.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18.11 MER18 repetitive element;
2004	15025		1.45	1.0E-12	AI871726.1	EST_HUMAN	wm5107.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element;
3085	16142	29053	0.78	1.0E-12	AF003991.1	NT	Homo sapiens testis-specific Testis Transcript Y.2 (TTY2) mRNA, partial cds
3085	16142	29054	0.78	1.0E-12	AF003991.1	NT	Homo sapiens testis-specific Testis Transcript Y.2 (TTY2) mRNA, partial cds
3888	16928	29836	31.6	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3888	16928	29837	31.6	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6078	18158		2.05	1.0E-12	U82928.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6159	18234		1.65	1.0E-12	Q8Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIA0081
6277	18349	32582	0.57	1.0E-12	BF642800.1	EST_HUMAN	EST00098 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847868 5'
6277	18349	32583	0.57	1.0E-12	BF642800.1	EST_HUMAN	EST00098 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847868 5'
6682	19739	33014	0.78	1.0E-12	AF228843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cyclic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7323	20284	33637	1.9	1.0E-12	AF168864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7357	20327	33675	11.35	1.0E-12	AI245533.1	EST_HUMAN	qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gbkM19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN) contains MER10.11 MER10 repetitive element;
7357	20327	33676	11.35	1.0E-12	AI245533.1	EST_HUMAN	qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gbkM19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN) contains MER10.11 MER10 repetitive element;
8834	21801	35220	0.48	1.0E-12	U66559.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2P, TCRBV7S2A1N4T, TCRBV13S9I/13S>
9053	22018	35444	1.16	1.0E-12	AA762323.1	EST_HUMAN	ac26a05.x1 Stratagene ovary (H37217) Homo sapiens cDNA clone IMAGE:557577 3'
12213	25052	38626	2.82	1.0E-12	AW062164.1	EST_HUMAN	h3374237 MAGO MAGO Homo sapiens cDNA
12434	25200		2.54	1.0E-12	AI735592.1	EST_HUMAN	w339h08.x1 NCI CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392085 3'
12582	25881		2.51	1.0E-12	AL163289.2	NT	Homo sapiens chromosome 21 segment HS21C068
1054	14100	27050	0.7	9.0E-13	AW082714.1	EST_HUMAN	x88107.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2560855 3' similar to contains MER28.12 MER28 repetitive element;
3643	16886		1.01	9.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3967	17007	29923	0.86	9.0E-13	AB028900.1	NT	Homo sapiens CST gene for cerebrosidase sulfotransferase, exon 1, 2, 3, 4, 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6660	22887		2.59	9.0E-13	N69653.1	EST_HUMAN	z22806.s1 Scores fetal liver spleen 1N1.S Homo sapiens cDNA clone IMAGE:263651 3'
718	13780	26714	6.78	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
718	13780	26715	6.78	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1855	14881	27877	3.1	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
8449	21418	34831	0.75	8.0E-13	A1884398.1	EST_HUMAN	wn31106.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8449	21418	34832	0.75	8.0E-13	A1884398.1	EST_HUMAN	wn31106.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
10595	23427		4	8.0E-13	U78027.1	NT	Homo sapiens Brn10's lysine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8127	21064	34462	0.58	7.0E-13	A1884398.1	EST_HUMAN	wn31106.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8127	21064	34463	0.58	7.0E-13	A1884398.1	EST_HUMAN	wn31106.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8576	21544		0.49	7.0E-13	Q95155	SWISSPROT	OLFACCTORY RECEPTOR-LIKE PROTEIN OLF2
12682	26350		5.56	7.0E-13	BE77823.1	EST_HUMAN	601465285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3966613 5'
2111	15128	28148	3.56	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3333	16384		0.74	5.0E-13	R78338.1	EST_HUMAN	y8280.x1 Scores placenta N12.H.P Homo sapiens cDNA clone IMAGE:145759 5'
3408	18457		1.35	5.0E-13	AA435773.1	EST_HUMAN	z177612.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element/contains element MER22 repetitive element
7050	20092	33390	0.7	5.0E-13	P08983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
11209	24163	37693	2.07	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1883	14908		6.02	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221099-001-s11 HT0224 Homo sapiens cDNA
2467	15471		2.44	4.0E-13	A5003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
4778	17798		0.99	4.0E-13	AA454054.1	EST_HUMAN	z48607.r1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:795489 5'
5687	13762	31831	4.39	4.0E-13	BE1189131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7413	20380	33731	1.05	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
							z477612.r1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763
7970	20814	34192	0.88	4.0E-13	AA431529.1	EST_HUMAN	G452763 COR1 mRNA
7989	20928		1.47	4.0E-13	N44261.1	EST_HUMAN	y33505.r1 Scores melanocyte 2NHR.HM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR.A32895
8193	22159	35587	1.2	4.0E-13	AL043910.1	EST_HUMAN	DKFZ444A0128_r1 434 (synonym: hsc3) Homo sapiens cDNA clone DKFZ444A0128 5'
9660	22796	36249	0.59	4.0E-13	AA078807.1	EST_HUMAN	7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11
10380	23303	36779	5.26	4.0E-13	AL289831.1	EST_HUMAN	q33205.x1 NCI_CGAP_K105 Homo sapiens cDNA clone IMAGE:1886945 3' similar to contains Alu repetitive element
11502	24444	37695	1.9	4.0E-13	AA435819.1	EST_HUMAN	z177610.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
11502	24444	37696	1.9	4.0E-13	AA435819.1	EST_HUMAN	z177610.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
181	13281		5.91	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
866	13922		3.35	3.0E-13	AA430310.1	EST_HUMAN	z889g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781408 5'
2378	15396	28410	1.65	3.0E-13	ALJ21736.1	NT	Homo sapiens Xq pseudautosomal region: segment 2/2
2487	15491		2.11	3.0E-13	ALJ6210.2	NT	Homo sapiens chromosome 21: segment HS21C610
2873	15676	28688	2.5	3.0E-13	BF372862.1	EST_HUMAN	CM8.FT0100-140700-242-808 FT0100 Homo sapiens cDNA
3201	16256		2.19	3.0E-13	AA745844.1	EST_HUMAN	db18402.x1 NC1 CGAP_K46 Homo sapiens cDNA clone IMAGE:1324035 3'
3514	16560	29484	0.9	3.0E-13	P10616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3514	16560	29485	0.9	3.0E-13	P10616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5618	18714	31872	0.64	3.0E-13	AA134017.1	EST_HUMAN	zn88110.r1 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;
5618	18714	31873	0.64	3.0E-13	AA134017.1	EST_HUMAN	zn88110.r1 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;
6106	19185	32404	0.71	3.0E-13	AW005639.1	EST_HUMAN	w285d02.x1 NC1 CGAP_Bn26 Homo sapiens cDNA clone IMAGE:2665890 3' similar to TR:O75139
8215	21184	34594	8.24	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDW protein (CDM), adrenoleukodystrophy protein >
8412	21381	34787	0.51	3.0E-13	AA352487.1	EST_HUMAN	EST180487 Activated T-cells XX Homo sapiens cDNA 5' and similar to similar to serine protease P100, Ralpha-reactive factor
8412	21381	34788	0.51	3.0E-13	AA352487.1	EST_HUMAN	EST180487 Activated T-cells XX Homo sapiens cDNA 5' and similar to similar to serine protease P100, Ralpha-reactive factor
10558	23430	36975	0.46	3.0E-13	AW595487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
11038	24000		2.69	3.0E-13	AJ064738.1	EST_HUMAN	HAC0539 Human fetal liver cDNA library Homo sapiens cDNA
11365	24332	37861	3.32	3.0E-13	BE063506.1	EST_HUMAN	CM6-BT0281-031189-087-003 BT0281 Homo sapiens cDNA
11924	24805	38598	1.54	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21: segment HS21C048
151	13254	28183	3.63	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDW protein (CDM), adrenoleukodystrophy protein >
1275	14310	27271	7.14	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3284	16347	29267	1.08	2.0E-13	BF431896.1	EST_HUMAN	hnb7605.x1 Soares_NSIF_PB_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3518	16564	29489	1.25	2.0E-13	AF106607.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4135	17107		1.61	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6245	19318	32548	4.71	2.0E-13	Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (SLAYER PROTEIN 1)
6247	20210	33538	6.49	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.1) exon 2
7265	19990	33267	0.59	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
7265	19990	33268	0.59	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10824	23745	37246	4.53	2.0E-13	5931868	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
12387	25165		5.43	2.0E-13	AW692155.1	EST_HUMAN	CGM-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
291	13365		1.49	1.0E-13	S74129.1	NT	FGF-1 fibroblast growth factor 1 [human; kidney, Genomic, 342 nt, segment 2 of 2]
889	13944		4.85	1.0E-13	AJ007673.1	NT	Homo sapiens LGMD2B gene
1339	14373	27343	1.39	1.0E-13	X67344.1	NT	H sapiens DMA, DM8, HLA-Z1, PP2, LMP2, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2037	15056	28074	2.43	1.0E-13	AA720574.1	EST_HUMAN	nm21g02.e1 NCI_CGAP_G0B0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13
4623	17644	30532	2.2	1.0E-13	BF340987.1	EST_HUMAN	THR1 repetitive element;
6596	19646	32915	0.61	1.0E-13	AA080732.1	EST_HUMAN	602038009F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185936 5'
8242	21211	34616	0.78	1.0E-13	AA577812.1	EST_HUMAN	YF335 seq F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8242	21211	34617	0.78	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.e1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu
10450	23372		0.82	1.0E-13	O15481	SWISSPROT	repetitive element; contains element MER24 repetitive element;
10684	23586	37084	0.49	1.0E-13	AF300701.1	NT	repetitive element; contains element MER24 repetitive element;
11707	24672	36249	10.13	1.0E-13	BF108755.1	EST_HUMAN	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
12206	25048		2.34	1.0E-13	AV716377.1	EST_HUMAN	Mus musculus osteoblastic protein tyrosine phosphatase mRNA, complete cds
12844	25454		3.21	1.0E-13	AJ271735.1	NT	7145e10.x1 Soares_NSF_P8_3W_OT_PA_P_ST Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER28 repetitive element;
333	13422	26345	3.14	9.0E-14	AA781159.1	EST_HUMAN	AV715377 DOB Homo sapiens cDNA clone DOBAIE03 5'
334	13423	26346	2.37	9.0E-14	AA781159.1	EST_HUMAN	Homo sapiens Xa pseudotumor region; segment 1/2
2608	15511		4.8	9.0E-14	AA961577.1	EST_HUMAN	424cd01.x1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
2597	15598	28617	1.03	9.0E-14	AJ133127.1	NT	aj24cd01.x1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
2597	15598	28618	1.03	9.0E-14	AJ133127.1	NT	RC4-C10322-080100-013-d08 CT0322 Homo sapiens cDNA
2784	15756	28777	6.84	9.0E-14	AB038162.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
							Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
							Homo sapiens TFF gene cluster for trefoil factor, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3126	18185	28094	5.43	9.0E-14	AW513296.1	EST_HUMAN	x54a05.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:2707833 3'
3252	13422	28345	0.67	9.0E-14	AA781189.1	EST_HUMAN	q24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1381232 3' similar to contains MER19.11 MER19
3511	18851	28759	7.15	9.0E-14	DT14547.1	NT	repetitive element:
4769	17807	30699	1.68	9.0E-14	AJ002153.1	NT	Human DNA, SINE repetitive element
3509	15555		1.44	8.0E-14	BE488263.1	EST_HUMAN	Sogulius oedipus gene for seminal vesicle secreted protein semogelin 1
3978	17018		3.46	8.0E-14	R76268.1	EST_HUMAN	h271c09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
8803	21126	34530	21.45	8.0E-14	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9918	22739	35192	3.1	8.0E-14	AA219316.1	EST_HUMAN	h272c03.r1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:629970 3'
11762	24690		1.52	8.0E-14	BE062558.1	EST_HUMAN	z117c10.s1 Strategene fetal retina 937202 Homo sapiens cDNA
12590	25284	31763	2.89	8.0E-14	AI688118.1	EST_HUMAN	wc92h08.x1 NCL CGAP_Oc3 Homo sapiens cDNA clone IMAGE:2328143 3'
1653	15873		3.89	7.0E-14	AW151673.1	EST_HUMAN	x87a10.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.12
9272	22238		0.51	7.0E-14	AL163265.2	NT	MER10 repetitive element;
367	13463	26381	16.94	6.0E-14	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C085
10181	23105	35587	2.54	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10181	23105	35588	2.54	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
620	13685	28603	5.23	5.0E-14	O83120	SWISSPROT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3683	16726		0.95	5.0E-14	AL163247.2	NT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MUL.TIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5093	18103	30979	1.39	5.0E-14	AIW073791.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
5611	18707	31864	4.84	5.0E-14	P08547	SWISSPROT	repetitive element;
1123	15656		1.95	4.0E-14	P04628	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1895	14920	27916	7	4.0E-14	AJ007873.1	NT	S-ANTIGEN PROTEIN PRECURSOR
3765	18607		1	4.0E-14	AA046502.1	EST_HUMAN	Homo sapiens LGM228 gene
4320	17349	30233	0.96	4.0E-14	N46328.1	EST_HUMAN	z687a08.r1 Soares_pregnat_uterus_NB-PU Homo sapiens cDNA clone IMAGE:387858 5'
8291	21260		0.6	4.0E-14	X87344.1	NT	yf7a1c1.s1 Soares_multiple_sclerosis_2NH-MSP Homo sapiens cDNA clone IMAGE:279180 3' similar to contains L1.13 L1 repetitive element;
							H. sapiens DMA, DMB, HLA-Z1, IPR2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	- Top Hit Descriptor
12905	25988		6.38	4.0E-14	AI695224.1	EST_HUMAN	wn08c03.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2495332 3' similar to contains Alu repetitive element.
950	14003	28955	4.69	3.0E-14	X05466.1	NT	R.nervosus mRNA for CP32 protein
4963	17978	30868	1.16	3.0E-14	7656864	NT	Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29) mRNA
6898	19950	33246	0.96	3.0E-14	AI420786.1	EST_HUMAN	hs91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:000519 000519 FATTY ACID AMIDE HYDROLASE.
6898	19950	33247	0.96	3.0E-14	AI420786.1	EST_HUMAN	hs91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:000519 000519 FATTY ACID AMIDE HYDROLASE.
7021	25675		0.51	3.0E-14	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7229	20251	33585	0.57	3.0E-14	AA386311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
9139	22105	35531	0.63	3.0E-14	N42165.1	EST_HUMAN	y07510.71 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:3913087 5'
11337	24287	37811	2.83	3.0E-14	BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
11568	18347	31293	6.06	3.0E-14	AW265354.1	EST_HUMAN	x045f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MFR9 repetitive element.
12824	28854		1.88	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C086
390	13465	26395	2.76	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
390	13465	26396	2.76	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
691	15847	26682	9.98	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2397	15404		1.88	2.0E-14	AW372668.1	EST_HUMAN	RC5-BT0377-09128-0314-D12 BT0377 Homo sapiens cDNA
2472	15476		1.4	2.0E-14	7657629	NT	Homo sapiens thalidomide tumor necrosis region protein 1 (TRDR1), mRNA
2531	15534	28554	2.2	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C089
2547	15548		1.03	2.0E-14	BE22432.1	EST_HUMAN	hs90g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR11 OFR repetitive element.
2983	15679		1.48	2.0E-14	P08548	SWISSPROT	Homo sapiens chromosome 21 segment HS21C089
5602	18698	31669	0.91	2.0E-14	BF380661.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5702	18797	31972	0.81	2.0E-14	AI312351.1	EST_HUMAN	IL2-H10072-240800-142-D07 UT0072 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1 L3 L1 repetitive element.
5809	18898	32082	3.16	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7067	20089		0.92	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-805 BN0072 Homo sapiens cDNA
7260	20282	33598	0.57	2.0E-14	4885709	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11) mRNA
7502	20467	33828	0.87	2.0E-14	P56169	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7751	20704	34072	21.51	2.0E-14	BE158761.1	EST_HUMAN	IL2-H10397-071288-024-D04 HT0397 Homo sapiens cDNA
7751	20704	34073	21.51	2.0E-14	BE158761.1	EST_HUMAN	IL2-H10397-071288-024-D04 HT0397 Homo sapiens cDNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10277	22202	36687	0.52	2.0E-14	AI978795.1	EST_HUMAN	wf56g10.x1 NCI CGAP_UH Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element
10783	23704	37203	0.53	2.0E-14	AV741948.1	EST_HUMAN	AV741948 CB Homo sapiens cDNA clone CBFBFBP4 5'
11133	24083	37622	3.94	2.0E-14	AW139900.1	EST_HUMAN	UHLB11-adv-a-10-U11 x1 NCI CGAP_Su03 Homo sapiens cDNA clone IMAGE:2718234 3'
12822	25857		1.71	2.0E-14	AF008191.1	NT	Homo sapiens putative G3 protein (G3E) gene, complete cds
1086	14113	27083	2.09	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1405	14438	27406	8.16	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1405	14438	27407	8.16	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2017	15088	28049	15.42	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2195	15210	28228	5.77	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2418	15426	28449	5.29	1.0E-14	AF001989.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2955	16013	28940	1.05	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-II)
3182	16237	29164	6.2	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-409_1 CT0432 Homo sapiens cDNA
3182	16237	29155	6.2	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-409_1 CT0432 Homo sapiens cDNA
3901	16941	29652	1.75	1.0E-14	AA682994.1	EST_HUMAN	ta08c12.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4500	17525	30410	2.07	1.0E-14	AW275652.1	EST_HUMAN	xq39H10.x1 NCI CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2763059 3'
5907	18993	32184	2.1	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
5831	25659	33176	11.02	1.0E-14	11437150	NT	Homo sapiens protein (mouse)-like 1 (PROML1), mRNA
6831	25659	33177	11.02	1.0E-14	11437150	NT	Homo sapiens protein (mouse)-like 1 (PROML1), mRNA
1579	14612	27584	1.78	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR-T), mRNA
2183	15198		1.37	9.0E-15	AF106779.1	NT	Homo sapiens transcription factor IG-HM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds, and L-type calcium channel $\alpha_2$
7738	20693	34056	4.28	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN (CONTAINS: CORE PROTEINS P15, P12, P30, P10)
8350	21319	34733	1.17	9.0E-15	BE903559.1	EST_HUMAN	601077750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3980186 5'
2822	13553		1.42	8.0E-15	BE261482.1	EST_HUMAN	601145632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7587	20356	33708	1.55	7.0E-15	BF035327.1	EST_HUMAN	601155631F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3662066 5'
10801	23722		2.45	7.0E-15	AW241988.1	EST_HUMAN	777002.T1 Sources_NEL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THRL2 THR repetitive element
996	14047	27001	6.55	6.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 22
6027	19110	32311	1.11	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cytosine-rich protein
6027	19110	32312	1.11	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cytosine-rich protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
410	13483	28418	5.24	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2771	15783	28784	2.05	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RbRef gene, and sodium phosphate transporter (NP73) gene, complete cds
3482	16528		1.08	5.0E-15	AW298817.1	EST_HUMAN	UHF3BWQ-4ip-g-10-c-U1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:2731219.3
11035	23959		2.27	5.0E-15	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06.5
427	13122	29020	3.54	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6822	19876	33165	0.88	4.0E-15	AB007870.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
11401	21088	34487	1.79	4.0E-15	AJ130864.1	NT	Homo sapiens mRNA for transcription factor
11401	21088	34486	1.79	4.0E-15	AJ130864.1	NT	Homo sapiens mRNA for transcription factor
4245	17274		6.54	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142.5 similar to ANF(CARDIODILATIN)
5057	18077	30959	0.87	3.0E-15	AA078037.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library/Homo sapiens cDNA clone 7P01F03
5057	18077	30959	0.87	3.0E-15	AA078037.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library/Homo sapiens cDNA clone 7P01F03
6986	20209		1.27	3.0E-15	Q64625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7495	20460	33819	3.89	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7495	20460	33820	3.86	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
10285	23210		2.86	3.0E-15	AA807128.1	EST_HUMAN	cc36a07.s1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1351784.3 similar to contains MER13.11 MER19 repetitive element;
11146	24106	37633	3.42	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
250	13347	26273	4.45	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
388	13454	26382	4.01	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
368	13454	26383	4.01	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2381	15389	28413	1.02	2.0E-15	BE350127.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3146256.3 similar to contains MER29.b3 MER29 repetitive element;
2381	15389	28414	1.02	2.0E-15	BE350127.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3146256.3 similar to contains MER29.b3 MER29 repetitive element;
4095	17129	30023	1.21	2.0E-15	AW238498.1	EST_HUMAN	3p28X01.x1 NCI CGAP_HNTO Homo sapiens cDNA clone IMAGE:2741621.3 similar to contains L1.13 L1 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4653	17874		2.73	2.0E-15	AI06835.1	EST_HUMAN	wf7008.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348923 3' similar to TR:Q61043 Q61043 NINEN. ;
6306	19377	32618	1.02	2.0E-15	BE62352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877268 5'
6306	19377	32617	1.02	2.0E-15	BE62352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877268 5'
7321	20262		1.42	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7486	20451	33810	2.64	2.0E-15	AA704195.1	EST_HUMAN	z17603.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7626	20585	33948	4.75	2.0E-15	W05064.1	EST_HUMAN	z178410.1 Soares_fetal_liver_NHL19W Homo sapiens cDNA clone IMAGE:288875 5' similar to
8117	21054	34451	0.87	2.0E-15	AL163247.2	NT	WP144F4.8 CD2227 TRANSPOSASE ;
9257	22223	35653	2.73	2.0E-15	D14547.1	NT	Homo sapiens chromosome 21 segment HS21C047
9427	22391	35829	0.74	2.0E-15	AA397758.1	EST_HUMAN	Human DNA, SINE repetitive element
9427	22391	35830	0.74	2.0E-15	AA397758.1	EST_HUMAN	z17608.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9759	22700	36157	1.19	2.0E-15	AW378465.1	EST_HUMAN	z17608.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9759	22700	36158	1.19	2.0E-15	AW378465.1	EST_HUMAN	CN04HT0244-201099-078-at12 HT0244 Homo sapiens cDNA
11187	24143		4.15	2.0E-15	AJ271735.1	NT	CN04HT0244-201099-078-at12 HT0244 Homo sapiens cDNA
12694	18339	31288	3.19	2.0E-15	AF223391.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12694	18339	31289	3.19	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2786	15777		2.95	1.0E-15	AI689984.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3025	18082	29005	1.93	1.0E-15	BE043584.1	EST_HUMAN	626105.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270746 3' similar to TR:Q13539 Q13539
3158	19214	28128	1.2	1.0E-15	P08547	SWISSPROT	MARINER TRANSPOSASE ;
5180	18198	31071	1.11	1.0E-15	AI694928.1	EST_HUMAN	NA4002.x1 NCI_CGAP_OG4 Homo sapiens cDNA clone IMAGE:269182 5'
6508	19572	32825	1.63	1.0E-15	T95763.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7205	20228		1.93	1.0E-15	BE074217.1	EST_HUMAN	wf8604.x1 NCI_CGAP_XG11 Homo sapiens cDNA clone IMAGE:2494560 3'
7239	19974	33272	0.76	1.0E-15	P39057	SWISSPROT	ye40410.s1 Soares_fetal_liver_spleen_NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains
8574	21542	34662	1.04	1.0E-15	AL163280.2	NT	MERS repetitive element ;
8763	21730	35152	4.51	1.0E-15	AL200978.1	EST_HUMAN	QY3-BT0560-270100-074-p05 BT0568 Homo sapiens cDNA
8763	21730	35153	4.51	1.0E-15	AL200978.1	EST_HUMAN	DYNEIN BETA CHAIN, CYLIARY
8394	22359	35789	0.49	1.0E-15	AL153207.2	NT	Homo sapiens chromosome 21 segment HS21C080
8394	22362	35793	1.5	1.0E-15	4507208	NT	Homo sapiens chromosome 21 segment HS21C090
							Homo sapiens chromosome 21 segment HS21C097
							Homo sapiens spermidine synthase (SRM) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9602	22606	36035	0.79	1.0E-15	Q39575	SWISSPROT	DYENIN GAMMA-CHAIN, FLAGELLAR OUTER ARM
9890	22917	36393	0.95	1.0E-15	AA84653.1	EST_HUMAN	chr37c03.s1 NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1458672 3' similar to contains L1.03 L1 repetitive element;
11169	24127	37657	4.18	1.0E-15	AF040383.1	NT	Homo sapiens major histocompatibility locus class III region
13008	25720	31612	9.25	1.0E-15	A1763944.1	EST_HUMAN	element;
4532	17555	30443	1.15	9.0E-16	4503168	NT	Homo sapiens cut. (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
11338	24288	37812	1.94	9.0E-16	F06693.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
5785	18878	32090	0.79	7.0E-16	4885120	NT	Homo sapiens chondrin (C-C motif) receptor 8 (CCH8) mRNA
7564	20527	33885	1.45	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
7564	20527	33886	1.45	7.0E-16	O88807	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
12357	25809		1.88	7.0E-16	TS4149.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
2151	15167		7.77	6.0E-16	AW972611.1	EST_HUMAN	rs28632.1 Stratagene lung (5337210) Homo sapiens cDNA clone IMAGE:118062 5'
1489	14522	27495	1.28	5.0E-16	AJ251154.1	NT	EST 1384702 IMAGE resequences; MAGL Homo sapiens cDNA
2689	15685	28702	2.52	5.0E-16	AA992176.1	EST_HUMAN	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
10414	23336	36821	0.48	5.0E-16	AL163246.2	NT	chr80.cd4.s1 Soares, total testis, Nb2HF8_Sw Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element;
11849	24732	38319	2.54	5.0E-16	BF217568.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
13044	25585		10.68	5.0E-16	11418127	NT	601685734F1 NIH MGCG_57 Homo sapiens cDNA clone IMAGE:4104128 5'
2288	15263	28421	1.64	4.0E-16	A6001523.1	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2288	15366	28421	2.21	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2 complete and partial cds
2288	15396	28422	2.21	4.0E-16	AW797168.1	EST_HUMAN	QVY1-UM0036-200300-115-902 UM0036 Homo sapiens cDNA
3471	15617	29438	3.94	4.0E-16	Q16653	SWISSPROT	QVY1-UM0036-200300-115-902 UM0036 Homo sapiens cDNA
4165	17197	30053	4.74	4.0E-16	BE093975.1	EST_HUMAN	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4165	17197	30054	4.74	4.0E-16	BE093975.1	EST_HUMAN	PMA-BT0650-010400-002-909 BT0650 Homo sapiens cDNA
7980	20919	34310	37.37	4.0E-16	AL163284.2	NT	PMA-BT0650-010400-002-909 BT0650 Homo sapiens cDNA
9550	22894	35042	0.97	4.0E-16	11423191	NT	Homo sapiens chromosome 21 segment HS21C084
12290	25106		2.41	4.0E-16	P08548	SWISSPROT	Homo sapiens hyalohyalin protein FLJ10324 (FLJ10024), mRNA
12392	25169	31816	2.11	4.0E-16	8912459	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12556	25336		1.36	4.0E-16	R18591.1	EST_HUMAN	Y9691.1.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30489 5'
133	13238	28169	1.24	3.0E-16	AW022862.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIA0571), mRNA d145c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2466376 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
133	13238	26170	1.24	3.0E-16	AW022862.1	EST_HUMAN	445501.Y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
466	13539		1.91	3.0E-16	AL046445.1	EST_HUMAN	DKFZp343P037.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp343P037 5'
476	13548		3.08	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1446	14479	27465	1.53	3.0E-16	Q26893	SWISSPROT	ZONADHESIN PRECURSOR
2888	15046	28968	3.94	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3953	16963	28909	0.96	3.0E-16	T08169.1	EST_HUMAN	ES-T06060 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBA13 5' end
3960	17020		0.77	3.0E-16	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3981	17021		1.06	3.0E-16	U03987.1	NT	Human BXP20 gene
5350	18455		1.11	3.0E-16	AA077225.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5698	18793	31956	1.2	3.0E-16	AF003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9005	21971	35392	4.92	3.0E-16	AL002836.1	EST_HUMAN	an98h05.x1 Stradiene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR12 THR repetitive element;
10250	23175		0.9	3.0E-16	BF960617.1	EST_HUMAN	602246838F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4332032 5'
10478	23400	36897	5.77	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13079	25961	31317	1.4	3.0E-16	AL043283.2	EST_HUMAN	DKFZp343L1623.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp343L1623 5'
973	14025		1.04	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078
2395	15402		1.32	2.0E-16	AA621761.1	EST_HUMAN	af66d04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2699	15695		1.25	2.0E-16	U03061.1	NT	Human GSAT-related endogenous retroviral LTR-like element
4207	17236	30123	1.14	2.0E-16	X89211.1	NT	H sapiens DNA for endogenous retroviral like element
6905	19957	33254	0.83	2.0E-16	Q31125	SWISSPROT	HISTIDINE-RICH PROTEIN KE4
7894	20923	34316	1.4	2.0E-16	AK70723.1	EST_HUMAN	H15a11.v1 NCI CGAP Gene4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element;
8300	21269	34631	1.86	2.0E-16	AI732837.1	EST_HUMAN	nz4706.x5 NCI CGAP_P112 Homo sapiens cDNA clone IMAGE:1280947 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 contains MER7 11 MER7 repetitive element;
9498	21466	34892	0.73	2.0E-16	BE59026.1	EST_HUMAN	762209.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8498	21466	34893	0.73	2.0E-16	BE59026.1	EST_HUMAN	762209.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
9872	21839	35261	0.75	2.0E-16	AW877214.1	EST_HUMAN	CN4-P170034-180200-506-a01 P170034 Homo sapiens cDNA
8872	18799	35262	0.75	2.0E-16	AW877214.1	EST_HUMAN	CN4-P170034-180200-506-a01 P170034 Homo sapiens cDNA
11274	24226	37762	1.86	2.0E-16	5902145	NT	Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA
186	13286	26210	2.57	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
382	13485		37.96	1.0E-16	A462892.1	EST_HUMAN	af3911.1.1 Soares fetal testis NB2H8.5w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element;
1988	15009	28014	2.22	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0148-070700-289-410 BN0148 Homo sapiens cDNA
5810	18900	32083	0.88	1.0E-16	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6574	19634		25.9	1.0E-16	U45983.1	NT	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds
6726	19782	33061	3.06	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7802	19934		6.75	1.0E-16	U45983.1	NT	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds
9638	22592	36031	1.06	1.0E-16	AW675951.1	EST_HUMAN	QV2-PT0012-040400-124-605 PT0012 Homo sapiens cDNA
3751	16793	29704	2.77	9.0E-17	AW900048.1	EST_HUMAN	CM1-NT1003-200300-153-407 NT1003 Homo sapiens cDNA
6886	19938		2.95	9.0E-17	A032964.1	EST_HUMAN	Q22x11.x1 NCL CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12 MER28 repetitive element;
8445	21414		5.47	9.0E-17	AW150257.1	EST_HUMAN	Xg49g12.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.12 OFR repetitive element;
10584	23509		2.3	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1020	14066		2.01	8.0E-17	AW690701.1	EST_HUMAN	QV0-OT0032-080300-155-001 OT0032 Homo sapiens cDNA
3907	16947		0.88	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5963	29642	31827	3.24	8.0E-17	BE172081.1	EST_HUMAN	MRO-HT0559-060300-003-604 HT0559 Homo sapiens cDNA
7490	20455		1.82	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFA0B07 5'
8019	20956	34349	0.54	8.0E-17	6733657	NT	Mus musculus dyf <sup>10n</sup> , exon, heavy chain 11 (Dnahc11), mRNA
1452	14485		2.63	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
5396	18489		3.14	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6845	19938	33183	7.34	7.0E-17	AF228643.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cyclic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
204	13305	26224	6.62	6.0E-17	AW683880.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
6446	19511	32781	1.8	6.0E-17	AW662772.1	EST_HUMAN	h181.d04.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978995 3' similar to contains L1.12 L1 repetitive element;
10855	23577	37074	0.54	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GPR7)
10929	23846		0.46	6.0E-17	W92331.1	EST_HUMAN	ze15f923.s1 Soares fetal heart NKH19W Homo sapiens cDNA clone IMAGE:359093 3'
421	13116	28014	3.22	5.0E-17	T64110.1	EST_HUMAN	yc09008.1 Stratiens lung (#637210) Homo sapiens cDNA clone IMAGE:796839 5'
7640	20787	34162	1.76	5.0E-17	T61043.1	EST_HUMAN	yc28504.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:109327 5'
9717	22745	36196	1.24	4.0E-17	AW129185.1	EST_HUMAN	x120d04.x1 NCL CGAP_Ki68 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11821	24704	38289	1.96	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12303	25114		2.02	4.0E-17	A1073546.1	EST_HUMAN	ov45804.x1 Scores: testis_NHT Homo sapiens cDNA clone IMAGE:1640288 5' similar to TRQ16530
1460	14522		1.72	3.0E-17	D14547.1	NT	Q16530 PMS3 MRNA, contains MER10.12 MER10 repetitive element ;
2108	15125	28144	1.22	3.0E-17	AW119123.1	EST_HUMAN	Human DNA, SINE repetitive element
3208	16283		1.66	3.0E-17	P35410	SWISSPROT	q98c09.x1 Scores: NFL_I, GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3656	16699	29814	1.33	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3656	16699	29815	1.33	3.0E-17	BE326522.1	EST_HUMAN	hw05004.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181969 3'
5088	18078		1.17	3.0E-17	BF511266.1	EST_HUMAN	hw05004.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181969 3'
							U1H-B14.seq-e-06-0.U1.st NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085043 3'
							z11402.81 Scores: fetal liver spleen 1NF1LS Homo sapiens cDNA clone IMAGE:292481 3' similar to contains
8911	21579	34695	1.16	3.0E-17	N68451.1	EST_HUMAN	PTRE.03 PTH3 repetitive element ;
10060	22987	36455	4.94	3.0E-17	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10746	23668	37184	0.73	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047.270700-283-412 BN0047 Homo sapiens cDNA
10746	23668	37195	0.73	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047.270700-283-412 BN0047 Homo sapiens cDNA
12266	25089		3.31	3.0E-17	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
353	13442	26397	3.4	2.0E-17	A1270080.1	EST_HUMAN	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1969622 3' similar to contains Alu repetitive element
354	13442	26397	3.97	2.0E-17	A1270080.1	EST_HUMAN	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1969622 3' similar to contains Alu repetitive element
980	14042		2.04	2.0E-17	AA722932.1	EST_HUMAN	zaps.c04.x1 Scores: fetal heart_NH-H19W Homo sapiens cDNA clone IMAGE:398751 3'
2453	15458	28479	2.3	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2453	15458	28480	2.3	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
							NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
2941	15989	28922	6.23	2.0E-17	P12038	SWISSPROT	Mus musculus ultra high sulfur keratin gene, complete cds
5440	18542	31452	1.8	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5440	18542	31453	1.8	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6395	19463		1.89	2.0E-17	AF050068.1	NT	Homo sapiens MHC class I region
6538	19886		1.66	2.0E-17	AL134881.1	EST_HUMAN	DKFZ762J0610.t1.762 (synonym: hme2) Homo sapiens cDNA clone DKFZ762J0610 5'
8133	21070	34469	0.85	2.0E-17	AB037839.1	NT	Homo sapiens mRNA for KIAA1418 protein, partial cds
8420	21389	34796	1.47	2.0E-17	Q96158	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLFS
8900	21767	35191	1.29	2.0E-17	AA300840.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
10228	23163	36643	2.35	2.0E-17	BE299888.1	EST_HUMAN	600944650F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960915 5'
10294	23189	36673	2.83	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10284	23189	36674	2.83	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047 Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10622	23544	37044	5.23	2.0E-17	D13391.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10745	23667	37162	0.98	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10745	23667	37163	0.88	2.0E-17	P98063	SWISSPROT	wee4d04.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10772	23693	37190	0.57	2.0E-17	A1798902.1	EST_HUMAN	wee4d04.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10772	23693	37191	0.57	2.0E-17	A1798902.1	EST_HUMAN	Homo sapiens nuclear factor of kappa light polypeptide gene enhanced in B-cells 1 (NFKB1) gene, complete cds
12066	25153		1.31	2.0E-17	AF213884.1	NT	
751	13812	26755	3.24	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1721	14751		1.35	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1782	14811	27797	4.54	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2124	15141	28158	1.95	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2343	15353	28374	2.43	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3591	16626		1.05	1.0E-17	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4162	17183		8.5	1.0E-17	R05942.1	EST_HUMAN	h384c05.x1 NCL CGAP_CW11 Homo sapiens cDNA clone IMAGE:2821312 3' similar to contains Alu repetitive element; contains LTRs; H1 LTR3 repetitive element;
5800	19660		0.68	1.0E-17	AW468468.1	EST_HUMAN	q685605.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743925 3'
6809	19893	33151	1.73	1.0E-17	A1165642.1	EST_HUMAN	q685605.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743925 3'
6809	19893	33152	1.73	1.0E-17	A1165642.1	EST_HUMAN	URIDINE PHOSPHORYLASE (UDRPASE)
7296	20268	33603	0.96	1.0E-17	Q116831	SWISSPROT	QV4-BT0268-101296-072-407 BT0263 Homo sapiens cDNA
8039	21905	35326	1.7	1.0E-17	BE062744.1	EST_HUMAN	QV3-BN0046-223300-129-c10 BN0046 Homo sapiens cDNA
10396	23289	39766	0.87	1.0E-17	AW596538.1	EST_HUMAN	QV3-BN0046-223300-129-c10 BN0046 Homo sapiens cDNA
11747	24632	38212	1.64	1.0E-17	Q28924	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN] hu25605.x1 NCL CGAP_Mer15 Homo sapiens cDNA clone IMAGE:3171104 3' similar to contains MER13.b1 MER13 repetitive element;
13104	25825		1.63	1.0E-17	BE221470.1	EST_HUMAN	q685605.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
9856	22782		2.96	9.0E-18	A4172167.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3500	16840	28747	1.87	8.0E-18	476897	NT	POLYPEPTIDE N-ACETYLGLUTAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGLUTAMINYLTRANSFERASE) (UDP-GALNAc:POLYPEPTIDE-N- ACETYLGLUTAMINYLTRANSFERASE) (GALNAc-T1)
3999	16939	— 22850	3.75	8.0E-18	Q07537	SWISSPROT	xy10504.x1 NCL CGAP_Prim1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbl.20868 90S RIBOSOMAL PROTEIN L4 (r-L4);
349	13438	26361	23.15	7.0E-18	AW316976.1	EST_HUMAN	

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
349	13438	26362	23.15	7.0E-18	AW316976.1	EST_HUMAN	xt1004.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb1.20868 60S
7677	20635	33997	0.96	7.0E-18	AW897542.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); RC3-OT0091-17030-011-403 OT0091 Homo sapiens cDNA
12769	13438	26361	2.67	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); xt1004.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb1.20868 60S
12769	13438	26362	2.67	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); xt1004.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb1.20868 60S
3306	16359	26278	1.26	6.0E-18	X717791.2	NT	Rattus norvegicus partial GAPDH-1 gene for glycolytic medium protease neoin L enhancer region
4777	17197		4.3	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC) Homo sapiens similar to high-mobility group (nonhistone chromosome) protein 4 (H. sapiens) (LOC83449), mRNA
8523	21561		2.64	6.0E-18	11428155	NT	mRNA
9691	21699	35082	0.57	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11469	24412	37691	1.54	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11657	24593	38160	2.09	6.0E-18	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IIP2, LIMP2, TAP1, LIMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
12527	26266	31805	2.65	6.0E-18	U67926.1	NT	Human acetylhydrolase (ACO2) gene, exon 4 hg85h11.x1 Scars, placenta, 80cweeks_2NHP85c9W Homo sapiens cDNA clone IMAGE:1893998 3' similar to contains Alu repetitive element
1150	14192	27144	17.8	5.0E-18	AI280214.1	EST_HUMAN	Human endogenous retrovirus HERV-P-147D
5345	18450	31321	0.99	5.0E-18	AF087913.1	NT	MR0-HT0161-221-099-202-006 HT0161 Homo sapiens cDNA
9070	22036	35459	5.53	5.0E-18	BE143312.1	EST_HUMAN	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11323	24273	37800	3.26	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11323	24273	37801	3.26	5.0E-18	10242378	NT	MR1-SN035-060400-001-g11 SN035 Homo sapiens cDNA
12649	28332		6.29	5.0E-18	AW897182.1	EST_HUMAN	AV69047 GLC Homo sapiens cDNA clone GLC03A02 3'
12890	25544		3.2	5.0E-18	AV690547.1	EST_HUMAN	hg36h04.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29 b3 MER29 repetitive element
125	13232	26160	1.04	4.0E-18	BE044076.1	EST_HUMAN	hg36h04.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29 b3 MER29 repetitive element
125	13232	26161	1.04	4.0E-18	BE044076.1	EST_HUMAN	hg36h04.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb1.26926 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN); w33p08.x1 NCL CGAP_Cot10 Homo sapiens cDNA clone IMAGE:2392095 3'
1729	14759	27744	1.61	4.0E-18	AA621814.1	EST_HUMAN	N-Acetyllactosaminide BETA-1,8-N-Acetylglucosaminyltransferase (N-
1306	14830		0.95	4.0E-18	AI738592.1	EST_HUMAN	ACETYLGLUCOSAMINYLTRANSFERASE) (BRANCHING ENZYME) (IGIT)
2211	15228	28247	1.1	4.0E-18	Q06430	SWISSPROT	

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2211	15226	28248	1.1	4.0E-18	Q06430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYL TRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (GN7)
3806	18846	29753	0.76	4.0E-18	A1581586.1	EST_HUMAN	er033006.x1 Basaloid colon HPLRB7 Homo sapiens cDNA clone IMAGE:1627138 3' repetitive element
5437	19538	31447	2.29	4.0E-18	A1017595.1	EST_HUMAN	u023606.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5437	19539	31448	2.29	4.0E-18	A1017595.1	EST_HUMAN	u023606.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
8178	21148		0.67	4.0E-18	AA746811.1	EST_HUMAN	nc04608.x1 NCL CGAP_AW1 Homo sapiens cDNA clone IMAGE:126888 similar to contains L1.12 L1 repetitive element
11348	24298	37828	4.22	4.0E-18	AA371807.1	EST_HUMAN	EST336933 Pituitary gland, subnucleated (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
850	13906	26985	24.96	3.0E-18	AA814196.1	EST_HUMAN	ad32ht11.s1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324881 3' similar to SWRS5_HUMAN
530	13963	26938	3.54	3.0E-18	BE08834.1	EST_HUMAN	P48782 4B5 RIBOSOMAL PROTEIN S5
3972	17012	26928	1.31	3.0E-18	AL16347.2	NT	CMG-BT0090-210300-298-407 BT0060 Homo sapiens cDNA
7003	20129	33444	8.43	3.0E-18	BE001671.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
11271	24223	37748	1.76	3.0E-18	BF218650.1	EST_HUMAN	PNC-BN0081-100300-001-008 BN0081 Homo sapiens cDNA
12774	25412		5.15	3.0E-18	AW022015.1	EST_HUMAN	601384886F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 5'
251	13348	26274	5.97	2.0E-18	AW839820.1	EST_HUMAN	df31ht12.y1 Morion Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
1155	14197		67.85	2.0E-18	BE256097.1	EST_HUMAN	QY1-L-70036-150200-070-407 LT0036 Homo sapiens cDNA
3140	16197	29107	1.27	2.0E-18	Q39575	SWISSPROT	60111432F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
5465	18395		3.85	2.0E-18	AA868610.1	EST_HUMAN	DYNEN GAMMA CHAIN, FLAGELLAR OUTER ARM
5584	18690	31644	3.39	2.0E-18	D14547.1	NT	ak33607.s1 Soares_teste_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR-O14577
5584	18690	31645	3.38	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A06 FROM TQ31, COMPLETE SEQUENCE. : Human DNA, SINE repetitive element
5978	19083		1.87	2.0E-18	BF347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6289	19361	32598	1	2.0E-18	X60459.1	NT	602021164F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156870 5'
6289	19361	32599	1	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6409	19477	32724	0.75	2.0E-18	BF352940.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
6451	19516	32787	4.42	2.0E-18	AW66583.1	EST_HUMAN	IL3-IT0019-220700-222-C12 HT0019 Homo sapiens cDNA
7070	20629	33993	0.72	2.0E-18	AA457619.1	EST_HUMAN	h94a091.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875984 3' similar to contains MER19.12 MER19 repetitive element
8487	21455	34872	0.52	2.0E-18	BE439524.1	EST_HUMAN	enad8d11.r1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838485 5' similar to TR:G61834 G61834 POLYPEPTIDE PR77

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10407	23329	36813	1.31	2.0E-18	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.12 MER10 repetitive element.
10407	23329	36814	1.31	2.0E-18	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.12 MER10 repetitive element.
11319	24269	37797	3.07	2.0E-18	AW47079.1	EST_HUMAN	ha33005.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2876488 3' similar to contains THR.b3 THR repetitive element.
12039	24914	38508	2.88	2.0E-18	AW151299.1	EST_HUMAN	x917409.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MERR.b2 MERR repetitive element.
12481	14197		3.97	2.0E-18	BE250697.1	EST_HUMAN	607114352FT NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355044 5' y64305.r1 Soares fetal liver spleen TNF.LS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element.
4445	17471		0.93	1.0E-18	T05406.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLC.DKE11 3'
5429	18532	31412	2.71	1.0E-18	AV553405.1	EST_HUMAN	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5650	18748	31974	1.87	1.0E-18	D00039.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5950	18748	31915	1.87	1.0E-18	D00039.1	NT	Homo sapiens chromosome 21 segment HS21C080
6597	19657	32629	1.33	1.0E-18	AL163280.2	NT	contains L1.11 L1 repetitive element.
8785	21752	35174	1.13	1.0E-18	AF148288.1	EST_HUMAN	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RbRef gene, and sodium phosphate transporter (NPT3) gene, complete cds
10259	23184	36689	4.28	1.0E-18	U91328.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
12412	25184	31821	6.49	1.0E-18	AF003528.1	NT	x11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element.
547	13618	26540	5.55	9.0E-19	AA281681.1	EST_HUMAN	x11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element.
548	13618	26540	4.1	9.0E-19	AA281681.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
8181	21151		5.71	9.0E-19	F08638.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
9036	22002	35423	2.84	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9036	22002	35424	2.84	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11462	24405	37953	3.37	9.0E-19	AB032689.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
12172	13618	26540	1.94	9.0E-19	AA281681.1	EST_HUMAN	x11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element.
1050	14098		1.31	8.0E-19	AW974802.1	EST_HUMAN	EST1387007 MAGE sequences, MAGN Homo sapiens cDNA
4433	17480		0.86	8.0E-19	F08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8488	21458	34973	1.04	8.0E-19	BET18636.1	EST_HUMAN	MR0-HT0404-210200-001-g08 HT0404 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2257	15271	26296	1.43	7.0E-19	4758139	NT	Homo sapiens DEAD(H) (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kd) (DDX6) mRNA
6598	19658	32930	1.95	7.0E-19	AF082690.1	NT	Rattus norvegicus cp151 mRNA, partial cds
7519	20484	33845	1.02	7.0E-19	P28444	SWISSPROT	Beta CRYSSTALLIN A2
10372	23295	36771	0.43	7.0E-19	A134495.1	EST_HUMAN	h601c03.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2652302 3'
12313	25980		3.26	7.0E-19	AA70584.1	EST_HUMAN	h601c03.x1 Scores, fetal liver, spleen, TNF.LS_S1 Homo sapiens cDNA clone IMAGE:435146 3'
3722	16833		1.8	6.0E-19	AW552300.1	EST_HUMAN	PMD-C10248-131099-001-001 C10248 Homo sapiens cDNA
4490	17515	30403	1.44	6.0E-19	P34966	SWISSPROT	OLFACTORY RECEPTOR 6 (M60)
4490	17515	30404	1.44	6.0E-19	P34966	SWISSPROT	OLFACTORY RECEPTOR 6 (M60)
4837	17854		1.47	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5094	18074	30954	1.29	6.0E-19	AL120817.1	EST_HUMAN	DKFZp762F192.1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZp762F192 5'
5958	19043	32242	4.88	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC56)
6342	19411	32652	0.69	5.0E-19	AW663302.1	EST_HUMAN	h177608.Y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
10760	23711	37213	0.78	5.0E-19	AJ267695.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11685	24747	38329	4.78	5.0E-19	AW183725.1	EST_HUMAN	x187002.x1 Scores, NF.L.T.GBC_S1 Homo sapiens cDNA clone IMAGE:2664171 3' similar to contains element MSR1 repetitive element
556	13626	26544	0.89	4.0E-19	AB007670.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIA00801
2891	15687	28704	1.69	4.0E-19	BF697362.1	EST_HUMAN	h6021309T01.NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4287674 5'
5470	18571	31481	1.05	4.0E-19	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3666	16905	28812	1.4	3.0E-19	Q25997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3666	16905	28813	1.4	3.0E-19	Q25997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4315	17344	30227	0.69	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4315	17344	30228	0.69	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4475	17501	30385	1.78	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADG Homo sapiens cDNA clone ADCAMA11 5'
5552	18457		0.63	3.0E-19	AF22467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7612	20572		1.81	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC33222), mRNA
9814	21276	34539	1.11	3.0E-19	X89685.1	NT	Mus musculus mRNA for TPOR33 protein
12552	25373		16.28	3.0E-19	AF165520.1	NT	Homo sapiens phorbol 1 protein (PBI) mRNA, complete cds
2607	15568	28588	27.04	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4474	17500		1.23	2.0E-19	AJ311783.1	EST_HUMAN	g811602.X1 NCI_CGAP_K165 Homo sapiens cDNA clone IMAGE:1915598 3' similar to TR:Q69386 Q69386 POLYUEN GENE;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6172	19247	32480	0.61	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZ008 5'
7561	20524	33682	0.72	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8673	21641	35068	0.35	2.0E-19	AA012854.1	EST_HUMAN	Zf34c09.r1 Soenae retina N2b-HR Homo sapiens cDNA clone IMAGE:360860 5'
10269	23164	36662	0.66	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OL22
482	13555		2.11	1.0E-19	BE40881.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
							X776p07.r1 Soenae adult brain N2b-HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2174	15190	28211	1.68	1.0E-19	H30795.1	EST_HUMAN	Human gene for Ah-receptor, exon 7-9
2726	15723		2.48	1.0E-19	D38044.1	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
2860	15920		4.26	1.0E-19	4758977	NT	al49b12.s1 Soenae testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12
3412	16460	26381	1.18	1.0E-19	AA834967.1	EST_HUMAN	MER37 repetitive element;
5168	18195		0.9	1.0E-19	AW117377.1	EST_HUMAN	xd88h10.v1 Soenae NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2804739 3' similar to contains L1.b2.L1.L1 repetitive element;
6193	18287	32502	2.73	1.0E-19	U12188.1	NT	Cryptolegus cuticulus sodiumdicarboxylate cotransporter mRNA, partial cds
6333	25995		0.63	1.0E-19	AA595827.1	EST_HUMAN	h22d03.s1 NC1_CGAP_P1 Homo sapiens cDNA clone IMAGE:953053 similar to contains L1.t1.L1 repetitive element;
7690	20834	34213	0.99	1.0E-19	U08813.1	NT	Cryptolegus cuticulus Na <sup>+</sup> /glucose cotransporter-related protein mRNA, complete cds
7890	20834	34214	0.99	1.0E-19	U08813.1	NT	Cryptolegus cuticulus Na <sup>+</sup> /glucose cotransporter-related protein mRNA, complete cds
8095	25694		0.71	1.0E-19	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
8793	21760	35192	1.72	1.0E-19	M84657.1	NT	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
9093	22056		2.74	1.0E-19	T89920.1	EST_HUMAN	y97302.r1 Soenae fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element;
10108	23032		0.97	1.0E-19	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10547	23469	36964	27.33	1.0E-19	AW812286.1	EST_HUMAN	RCU-ST0174-19109-031-003 ST0174 Homo sapiens cDNA
10557	23479	36974	2.1	1.0E-19	N44831.1	EST_HUMAN	Y31c09.r1 Soenae melanocyte 2NBHr Homo sapiens cDNA clone IMAGE:272872 5'
11609	24694		3.69	1.0E-19	AW023137.1	EST_HUMAN	df49h01.v1 Morton Fetal Cerebellar Homo sapiens cDNA clone IMAGE:2487000 5'
6803	19857	33143	2.45	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6803	19857	33144	2.45	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7761	20714	34084	1.31	8.0E-20	A0221371.1	EST_HUMAN	q98609.x1 Soenae NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7761	20714	34085	1.31	8.0E-20	A0221371.1	EST_HUMAN	q98609.x1 Soenae NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3289	16342	26263	0.72	7.0E-20	BF328453.1	EST_HUMAN	PMA-AN0096-050900-003-gd AN0096 Homo sapiens cDNA
7188	18419	31220	5.56	7.0E-20	AL138120.1	EST_HUMAN	DKFZp547D082.r1 547 (synonym: hfb7) Homo sapiens cDNA clone DKFZp547D082 5'
8841	21808	35227	9.11	7.0E-20	AA557657.1	EST_HUMAN	146c04.s1 NC1_CGAP_P1 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8841	21808	35228	9.11	7.0E-20	AA587657.1	EST_HUMAN	n46c04.x1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER28b2 MER29 repetitive element;
12023	24898		6.31	7.0E-20	6912633	NT	Homo sapiens ribosomal protein L13a (RPL13A) mRNA
3568	16613	28535	3.93	5.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4301	17330	30210	2.88	6.0E-20	BE62343.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4828	17647		1.05	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HIC Homo sapiens cDNA clone HTCCBTAD01 5'
7322	20283	33636	1.19	5.0E-20	AF075301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
8277	21248	34857	5	5.0E-20	W90525.1	EST_HUMAN	z778d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;
8277	21248	34857	5	5.0E-20	W90525.1	EST_HUMAN	z778d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;
8440	21409	34822	0.79	5.0E-20	BE105980.1	EST_HUMAN	MR3-H10497-150200-113-g01 HIT0437 Homo sapiens cDNA
9187	22153	35582	1.24	5.0E-20	AB028174.1	NT	Mus musculus IMAN-g mRNA, complete cds
9187	22153	35583	1.24	5.0E-20	AB028174.1	NT	Mus musculus IMAN-g mRNA, complete cds
9800	21123		0.93	5.0E-20	O60809	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
1624	14657	27636	1.73	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS2TC047
5732	18826		0.89	4.0E-20	Q96880	SWISSPROT	HISTONE H2B C (H2B/C)
8258	21227		5.27	4.0E-20	AI874352.1	EST_HUMAN	z59a003.x1 NCI_CGAP_Ox33 Homo sapiens cDNA clone IMAGE:2283396 3'
10865	23785	37286	1.9	4.0E-20	AW937469.1	EST_HUMAN	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA
2149	15165	28181	0.91	3.0E-20	U03888.1	NT	Human BXP21 gene
4237	17266	30153	1.63	3.0E-20	P23273	SWISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN I14
4855	17676	30582	1.43	3.0E-20	AA037616.1	EST_HUMAN	z438512.s1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element;
9287	22253		3.32	3.0E-20	DT4547.1	NT	Human DNA, SINE repetitive element
10684	23906	37099	0.68	3.0E-20	BF185264.1	EST_HUMAN	601843561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4664343 5'
11024	23989		1.59	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11840	24723	38308	8.22	3.0E-20	AI284244.1	EST_HUMAN	q700d02.x1 NCI_CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1664803 3' similar to contains Alu repetitive element;
11840	24723	38309	8.22	3.0E-20	AI284244.1	EST_HUMAN	q700d02.x1 NCI_CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1664803 3' similar to contains Alu repetitive element;
12329	25130	31649	4.15	3.0E-20	BE868422.1	EST_HUMAN	601514190F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
831	13888		33.91	2.0E-20	AV303868.1	EST_HUMAN	x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW:R65_MOUSE P97461.403 RIBOSOMAL PROTEIN S5.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1113	14157	27107	3.88	2.0E-20	AA516335.1	EST_HUMAN	ng98109.s1 NCL CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR-G1224068
							G1224068 ORF2: FUNCTION UNKNOWN. ;
1113	14157	27108	3.88	2.0E-20	AA516335.1	EST_HUMAN	ng98109.s1 NCL CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR-G1224068
							G1224068 ORF2: FUNCTION UNKNOWN. ;
2828	13888		15.67	2.0E-20	AW303868.1	EST_HUMAN	x22410.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2781008 3' similar to SW_RSS_MOUSE
4983	17998	30895	4.76	2.0E-20	Q28983	SWISSPROT	P91461 40S RIBOSOMAL PROTEIN S5. ;
4883	17998	30897	4.76	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
8455	21424	34840	0.6	2.0E-20	AA330457.1	EST_HUMAN	EST180326 Liver III Homo sapiens cDNA 5' end
8545	22508	35957	7.56	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
8545	22508	35958	7.56	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12703	25714	31611	3.98	2.0E-20	H55371.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
2029	15822	28093	4.32	1.0E-20	AA281961.1	EST_HUMAN	211d06.11 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
							MER19 repetitive element. ;
4487	17489	30380	1.04	1.0E-20	BF115188.1	EST_HUMAN	hr6406.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1
7079	20100	33411	1.04	1.0E-20	AF049567.1	EST_HUMAN	repetitive element. ;
8518	22481	35626	2.24	1.0E-20	11418491	NT	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
							Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
11878	24761	38246	2.11	1.0E-20	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12458	25215		3.09	1.0E-20	AA420483.1	EST_HUMAN	nc00083.r1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:745684 similar to contains L1.13 L1
2923	15981		1	9.0E-21	AJ003514.1	EST_HUMAN	repetitive element. ;
12175	25023		3.77	9.0E-21	AW888189.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIp12-BJ21
							RC3-NN0098-000500-021-B03 NN0098 Homo sapiens cDNA
9163	22129		1.13	8.0E-21	AW674891.1	EST_HUMAN	b530402.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW_NIAM_HUMAN
11866	24748	38330	4.38	8.0E-21	AA809411.1	EST_HUMAN	085168 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR ;
12342	25140		2.64	8.0E-21	O21330	SWISSPROT	ab7106.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
2032	15099	28115	1.59	7.0E-21	P15800	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2032	15099	28116	1.59	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ) (LAMININ CHAIN B3)
3718	18759	28671	0.63	7.0E-21	AL163300.2	NT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ) (LAMININ CHAIN B3)
4283	17312		5.22	7.0E-21	AA046502.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
6573	19633	32900	0.81	7.0E-21	AL163218.2	NT	2617405.r1 Soares_pregnant_uterus_NHPTU Homo sapiens cDNA clone IMAGE:457658 5'
							Homo sapiens chromosome 21 segment HS21C018